SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:		Examiner # :	Date:
Art Unit:	Phone Number 30	Senal Number:	
Mail Box and Bldg/Room	n Location:	Serial Number: Results Format Preferred (circle):	PAPER DISK E-MAIL
f more than one searc	h is submitted, please	prioritize searches in order of ne	ed. ********
Please provide a detailed state nelude the elected species or ittlity of the invention. Defii	ement of the search topic, and structures, keywords, synony	describe as specifically as possible the subjects, and registry numbers, and registry numbers, and respectal meaning. Give examples or relevan	ect matter to be searched ombine with the concept or
Title of Invention:			
Inventors (please provide f	ull names):		
Earliest Priority Filing D	Date:		
*For Sequence Searches Only appropriate serial number.	* Please include all pertinent in	formation (parent, child, divisional, or issued p	atent numbers) along with the

PTO-1590 (1-200Q)

STIC-Biot ch/ChemLib

Q46429

From: Sent: To: Subject: Pak, Michael Monday, July 09, 2001 8:21 PM STIC-Biotech/ChemLib 09/276,935 sequence search

Sequence search - 2 month amendment App. #: 09/276,935 Result format: Paper. Title: an orphan nuclear receptor Please . search:

Search commercial database and interference.

Search SEQ ID NO:13 and 14 Reverse translate seq id no: 14.

Thanks,

Mike Pak

Michael D. Pak (703)305-7038 CM-1; Rm. 10E13 AU 1646 - USPTO

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 1E01 TEL: 308-3534

Technical Info. Specialist

CM1 1E01 TEL: 508-3534

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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 1	Score 2146	Match 100.0	Ouery Match Length DB 100.0 2146 88	DB 84	ID AF061056	Description AF061056 Homo sapi
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ω	2115.4	98.6	3057	10	E32709	E32709 Novel
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7	1866.6	87.0	2802	88	AF084644	AF084644 Home
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	aology, Glaxo Wellcome, 5	Willson,T.M., Moore,J.T. and	that regulate CYPHA4 gene expression and cause drug interactions J. Clin. Invest. 102 (5), 1016-1023 (1998) 9835173	s activated by compounds	: Enteleostomi e: Homo.		RI 20 JAN-1999 mRNA, complete eds.			230425 H.sapiens m AR009748 Sequence	AX099111 Sequence	AX099118 Sequence	AX099107 Sequence E14585 Human mRNA	AX099105 Sequence	AX099116 Sequence AX099103 Sequence	091846 Xenopus lae AB037673 Paralicht	E14584 Rat mRNA is	ABO37674 Paralicht	X75163 X.laevis mk AX099122 Sequence	J03258 Human vitam U12641 Coturnix ja	AF025250 Homo sapi X67482 H.sapiens m	AF011356 Gallus ga	AX099119 Sequence	AX099115 Sequence	AY007189 Homo sapi	AF276753 Gallus qa D31969 Mouse mRNA	E32706 Novel nucle	AF188476 Oryctolad AC069444 Homo sabi	AF031814 Mus museu AF151377 Rattus no	AF182217 Oryetolad	E32702 Novel nucle

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                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ009936
AJ009936.1 GI:5852062
nuclear hormone receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-JUL-1998) Heard D. Genetics, Novo Alle, DK-2880, Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSAJ9936 4448 bp mRNA PRI 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heard, D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vissing,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heard, D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Hum.
                                                                                                                                                                                                                                                                      receptor PXR/SXR and
       ATTEMS LATTON - "MDDRGEVQAKNILDDNSPRGDEANLEVREKESWHHTDEVHCEDTE SVPGKPSVNADEEVGGPGICRVCGDKATGYHFNVMTCEGCKGFFRKAMKKNARLRCPF RKGACE ITRKTRRQCQACRERKCLESGKNEM INSUEAVEERRSTUDE LGVQGLTEDGKMMI RELIMADAUMKTEDTTFSHFKNEK IDGVLESSGELDESLQAPS REE AAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPDADSGGKEIFSLLDHMALMSTYMFKG ILSFAKVISYFRDLPIEDDISLLKGAAFELCQLFKNIYVPNAETGTMERGRLSYCLEDT AGGFQQILLEPMLKFHYMLKKIQLHEEHYVLMQAISLFSPDRRGVLQHFKVUDQLQEQF ATTLKSVIECNRPQPAHRFLFLKIMAMLTELRSINAOHTQRILRIQDIHFFATPLMQE LEGITGS
                                                                                                                                                                                                                   /note-"isoform with longer A/B domain, translation initiates at GUG-1771 5 fold less efficiently than CUG-1840"
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                      /codon_start=1
/transl_except=(pos:1771.
/product="nuclear hormone"
                                                                                                                                                                                                                                                                                                                         /tissue_type="liver"
/tissue_type="intestine"
/tissue_type="colon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :
                                                                                                                                                                                                                                                              1771. .3144
/qene-"PRR1"
                                                                                                                                             /protein_id="CAB55490.1"
/db_xref-"GI:5852064"
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                                                                                                                                                                           .1773, ad:Met)
receptor PRR1-C*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor; PKR1
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eggaagggegeet gegagat.eaceeggaagaeeeggegaeagt geeaggeet geegeet.g
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/hote "tull length receptor"
/roote "tull length receptor"
/roote "tull length receptor"
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/roote "tull length receptor"
/product "nuclear hormone receptor Pkkl-A"
/product "nuclear hormone receptor Pkkl-A"
/product "nuclear hormone receptor Pkkl-A"
/product "tull blaze Stable"
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GDKATGYHENNETCEGCKGFFKRAMKKNAKLIG-VEKKGCELITEKTRQCVQACKLEKC
GDKATGYHENNETCEGCKGFFKRAMKKNAKLIG-VEKKGVGKTKDLKSLKYSLQLKGE
FEDTTYSHEKNERLPGVLSSGCELPESIJQAPSREEAKNSQVRKDLCSLKYSLQLKGE
FEDTTYSHEKNERLPGVLSSGCELPESIJQAPSREEAKNSQVRKDLCSLKYSLQLKGE
FOSVWNYKPPADSGGKEIESLLPHMADMSTYNEKGILESAKVISYFRDLFIEDGISLL
KGAAPELCQLKENTVPNAETGTWEGGRLSYCLEDTAGGFQGLILEDMLKFHYMLKKIQ
LHEEBYVLMQAISLESEDVRGVJJOHRVVJQLQEGFATTLKSY LECNRPQBAHRELFIK
RAMMITELRS NAQBTQRKLIKIQDIHPEATPLMQELFGITGS"
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Jun,Y.Y.S.S. and Naito.
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JAPAN TOBACCO INC
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Submitted (19–AUG-1998) Cell and Molecular Biology, Medical Nobel
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/protein_id="AAC64558.1"
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Mammalia; Eutheria; Primates; Catarrhin; (bases 1 to 324)
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Novel nuclear receptor protein, its gene patent: JP 1999127872-A 9 18-MAY-1999; JAPAN TOBACCO INC
                                                               Eukaryola: Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
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GTTSFAKVTEVERDDJESLKKGAAFELGOLRFNTYFNAETGTMEKTRLSYCLED
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VFNAETGTWECGRLSYCLEDTAGGFQOLLLEPMLKFHYMLKKLJLHEEEYVLMOATSL
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/protein_id≠"CAB55492.1"
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                                        Direct Submission Submitted (19-AUG-1998) Cell and Molecular Biology, Medical Nobel
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Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2802)
                                                                                                                                              Identification of a human nuclear receptor defines pathway for CYP3A induction Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12208-12213
                                                                                    Bertilsson, G.,
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FFRRAMKRNAKLGCPFEKGACELITKNTRKQCQACRLKKCLESGNKKEMINSDEAVER
RALLKRKKSERTGTOPLGVGGITEEOBMMIRELMDAOMKTDTTYSHFKNFRLPGVIS
SGCELPESLQAPSREEDAKMSQVRKDLCSLKYSLQLAFGTDTTYSHFKNFRLPGVIS
SGCELPESLQAPSREEDAKMSQVRKDLCSLKYSLQLAFGEGSVVNYKPPADSGGKEIF
SLLPHAADMSTYMFKGIISFAKVISYFRDLFIEDQISLLKGAAEBLQULRNTVENAE
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OS HOMO SAPIENS
PN JP 199127872
PD 1H-MAY-1998 JI
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PR 2UN YAMAMOTO.)
PC C12N15/09, C071
G01N33/53,
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Mammalla; Entheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1374)
Jun.Y.Y.S.S. and Naito.
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Patent: JP 1999127872-A 2 18 MAY-1999;
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G01N33/53, PC G01N33/566//(C12 C12P21/02,C12R1:19), PC C12N15/00, (C12N1 PG C12N15/00, (C12N1 PG CDS)
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Jun,Y.Y.S.S. and Naito.
Novel nuclear receptor protein, its gene and utilization
Patent: JP 1999127872-A 3 18-MAY-1999;
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Jun, Y.Y.S.S. and Naito.
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Mammalia: Butheriu: Primates: Catarrhini: Hominidae; Homo.
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                      Research Institute, 10550 North Torrey Pines Ed., La
Location/Qualifiers
                                                                                 Submitted (01-SEP-1999) Division of Biochemistry,
                                                                                                                                                                                                                                  Rabbit pregnane X receptor is activated by Drug Metab. Dispos. 28 (5), 529-537 (2000)
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Mammalia: Eutheria: Laqomorpha: Leporidae: Oryetolagus.
                                                                                                                    Direct Submission
                                                                                                                                             Savas, U., Wester, M.R.,
                                                                                                                                                                      2 (bases 1 to 1895)
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                                                                   tgtggggacaaggccactggctatcacttcaatgtcatgacaxqtgaaggatgcaagggc
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/note="PXR"
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HLADMSTYMFKGIINPAKVISVERDLPIEDQISELKGATLELCLLRFNTVFNAETGTW
ECGRLSYCVEDPEGGFQQLLVDPLLKFHYMLKKLQLHKEEYVLMQAISLFSPDRPGVV
QREVVDQLQERFAITLKAYIECSRPQPTHRFLFLKIMAVLTELRTINAQHTQRLLRIQ
DTHPFAITPLMRELFSTTDD*
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/protein_id="Anaba4426.1"
/protein_id="Anaba4426.1"
/db_xref="GI:5853354"
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KRKKREHMEAQPPGMQGLTGEQRMIIEELMDAQMKTFDTTFSHFKNFRLPEVLGSGCE
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/note="PXR; nuclear receptor subfamily 1 group I
zinc-finger protein; transcription factor"
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/strain-"breed New Zealand white:
/db_xref-"taxon.9986"
/tissue_type="kidney"
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Submitted (29-ocn-1997) Department of Molecular Endocrinology,
Glaxo Wellcome, 5 Moore Drive, RTP, NC 27709, USA
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Jones,S.A., McKee,D.D., oliver,B.B., Willson,T.M.,
Zetterstrom,R.H., Perlmann,T. and Lehmann,J.M.
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444 c. 468 q. 348 (
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McKee, D.D., Tomkinson, N.C., LeCluyse, E.L., Lambert, M.H.,
Willson, T.M., Kliewer, S.A. and Meore, J.T.
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The pregnance X receptor: a promiscuous xenobiotic receptor that has diverged during evolution
Mel. Endocrinol, 14 (1), 27-49 (2000)
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84.7%;
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                                     Score 991.4; DB 7;
Pred. No. 5.9e 217;
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        Indels
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843 GTCCTACTGCGTGGAAGACCCTGAAGGAGGCTTCCAGCAACTTCTTGTGGACCCCTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 COGGGACAAGGCCAAFGGTTACCACTTCAACGTCCTGACATGTGAAGGCTGCAAGGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         traactgagatteaacaeagtgfteaacgeggagaetggaacetgggagtgtggeegget
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        get geragaageaat tegeeat taetetgaagteet aeut tguutgeuut eggeeeeagee
                                                                                    GGCCATCTCCCTTTTCTCCCCAGACCGCCCAGGTGTGGTGCAGCGTGAAGTGGTGGACCA
                                                                                                      ggecatefeeefetteteeeeggaeeggeeaggfgfgetgeageaeegegtggfggaeea 1394
                                                                                                                                                                             GAAATTCCACTACATGCTGAAGAAGCTGCAGCTGCACAAGGAGGAGTACGTGCTGATGCA
                                                                                                                                                                                                qaaalteeaetaeatqetqaaqaqetqeaqetqeatqaqaaqaqaqtatqtqetqatqea 1334
                                                                                                                                                                                                                                                                                    COTOCTUAGAT TOAACACOGTGTTCAACGCAGAGAGTGGGCACTTGGGGAGTGTGGGTCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUACATUTCAACCTACA FGTTCAAAGGCATCATCAACTTTGCTAAAGTCATCTCCTACTT 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1515 tgctcaqcacacccaqcqqctqctgcgcatccaggacatacacccctttqctacqcccct 1574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1455 tgeteataqqttettgtteetgaaqateatygetatgeteaeegaqoteegaqqateaa 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1695 tgccaagag 1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1203 CATGCGGGAGCTGTTCAGCACCACACAGATGACTGAGGGCTGCTTTTTGGGCTAGGCCTCAA 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1083 CACCCACCGCTTCCTGTTCCTGAAGATCATGCCCGTCCTCACTGAGCTTCGTACTATCAA 1142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muzny, D.M., Adams, C.C., Bailey, M., Barbaria, J., Blankenburg, K.,
Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
David, R., Deigado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
Uugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,
Uugan-Rocha, S., Durbin, K.J., Fernandez, G., Ferraguto, D.,
Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hoques, M.,
Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M.,
Kelly, S., Kondejewski, N., Konq, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarde, O., Liu, J., Liu, W., Logan, O., Lozadoo, R.J., Lu, J.,
Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S.,
Oswal, G., Parish, B., Paxton, S., Paylon, B., Perez, L., Pu.L.,
Oswal, G., Parish, B., Paxton, S., Stamps, A., Sucgang, R.,
Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, O., Wahbah, M.,
Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A.,
Gibbs, R., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TECCTTETE 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aqaqqcaqccaqacccagagccctctgagccgccactcccqqqccaaqacagatgqacac 1694
                                                                                                                                                                                                                                                                                                              of Molecular and Human Genetics, Baylor College of Medicine, One Plaza, Houston, TX 77030, USA on Aug 7, 2000 this sequence version replaced gi:8699996.

Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
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1 (bases 1 to 160185)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, 34 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-MAY-2000) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 160185)
                                                                                              Center project name: HMTQ Center clone name: RPl1-169N13
Chemistry: Dye-primer Bodipy: 6% of reads
                             Sequencing vector: M13: L08821
                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                         Web site:
                                                                                                                                                                                                                                                   Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submission
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                                                                                                                                                                                                                      http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                     Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primates; Catarrhini; Hominidae; Homo
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 34 contiqs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemistry: Dye-terminator Bid Dye: 94% of reads Assembly program; Phrap; version 0.990329
Consensus quality: 132114 bases at least 040
Consensus quality: 142928 bases at least 030
Consensus quality: 147607 bases at least 030
Estimated insert size: 148422; sum-of-contius estimation Quality coverage: 0x in 020 bases; sum-of-contius estimation Quality coverage: 3.3x in 020 bases; sum-of-contius estimation
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Best Local Similarity 98.4%; Pred. No. 1.5e-146;
Matches 689; Conservative 0; Mismatches 11; Indels
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Search completed: July Job time: 15227 sec 11, 2001, 16:32

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Post-processing: Minimum Match 0%
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Copyright (c) 1993 - 2000 Compugen Ltd.
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23	236	11.0	3382	19	AAV18518	
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26	188.6	8.8	1404	20	AAX16597	Human vitamin D re
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38	97.6	4.5	2030	17	AAT18996	
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42	91.4	<u>م</u> س	2928	20	AAV64991	2
43	1	<u>4</u> 3	2940	10	AAN90124	DNA of clone phRAR
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Hum	Human pregnane	×	receptor		(hPXR) encoding DNA.	
Human;	Human; nuclea	nuclear receptor:	ır receptor; pregnan 450 mono-oxygenase:	pre	pregnane X receptor; PXR;	CYP: CYP3A4;
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Homo	o sapiens	ıs.				

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New human pregnane X receptor, used to identify specific modulators agents that induce expression of cytochrome P-450 mono-oxygenase
                                                                                                                  W09948915-A1
                               P-PSDB; AAY42691.
                                      WPI; 1999-601202/51.
                                                  Kliewer SA, Willson TM
                                                               (GLAX ) GLAXO GROUP LTD
                                                                            27-MAR-1998;
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Claim 4; Fig 1A-D; 69pp; English.

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The nucleic acid sequence was isolated from a human adult cDNA
library using a swellfish ANO23 delated probe. The protein can
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N.B. The specification specifically claims the VDRR nucleic acid and
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The present sequence encodes a human intranuclear receptor protein The nucleic acid sequence was isolated from a human adult cDNA library using a swellfish ANO23 derived probe. The protein can be used for the development of drugs and diagnosis and treatment
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be used for treating metabolic, proliterative or inflammatory conditions by introducing them into a mammal. The introduced nucleic acid is then capable of transforming a cell in vivo and then polypeptide is expressed A substance affecting VDRR signal transduction, such as an agonist or antagonist can be used for the manufacture of a medicament for treating

malian tumours, hyperproliterative skin disorders or hyperthyroidism. Nucleic acid vectors encoding for expression of a VDRR polypeptide can

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Claim 10; Fig 1A; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            phytoestrogen; calcium-channel blocker; steroid toxicity; tuberculosis;
breast cancer; osteoporosis; Cushing syndrome; virilism; hirsutism;
polycystic ovarian disease; cancer; colorectal; prostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX89080 standard;
                                              New steroid and xenobiotic receptor, used to identify modulators for controlling metabolism of steroids and xenobiotics, e.g. reducing
                                                                                                                                      Blumberg в, Evans RM
                                                                                                                                                                                                 09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human steroid and xenobiotic receptor (SXR) encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY21799
                                                                                                                                                                                                                                 08-JAN-1999;
                                                                                                                                                                                                                                                             15-JUL-1999.
                                                                                                                                                                                                                                                                                          W09935246-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear receptor; SXR; steroid and xenobiotic receptor; RXR; human; retinoid X receptor; P450 gene; steroid hormone; steroid metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-1999 (first entry)
                                                                                                                                                                   (SALK ) SALK INST BIOLOGICAL
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                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 583..1887
                                                                                                                                                                                                                                                                                                                     /transl_except= (pos:1261..1263, aa:Xaa)
/note= "Xaa= unknown; the start codon is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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transcription through response elements present in steroid-inducible P450 genes, in response to a wide variety of natural and synthetic steroid hormones and (iv) is prominently expressed in liver and intestine. SXR requilates expression of catabolic enzymes, in response to many different steroids, and thus affects metabolism. SXR is a broad specificity, low-
                                                                                                                                                                                                               Also, modulating endogenous SXR is used to treat disease, particularly an agonist is used where endogenous steroid levels are excessive (c.g. Cushing syndrome; virilism and hirsutism in women; polycystic ovarian disease; 11 beta-, 17 or 21-hydroxiase deficiency; 3 beta-hydroxystoroid dehydrogenase deficiency, or breast, colorectal or prostatic caucer), while antagonists are used where endogenous storoid levels are too low. Cells that express SXR are used to identify compounds likely to be
                                                                                                                                                                                                                                                                                                                                                                                                                                         cases of tuberculosis (treated with rifampin and related compounds), breast cancer (treated with tamoxifen, raloxifen etc.) or osteoporosis (treated with Vitamin K), or to slow metabolism of therapeutic steroids
                                                        encoding the SXR polypeptide
                                                                                       are used in immunohistochemical testing for studying distribution/expression density of SXR, also for diagnosis and therapeutically as antagonist. The present sequence represents the longest SXk cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          steroids particularly phytoestrogens or calcium channel blockers, to reduce steroid toxicity in subjects being treated with steroids, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circulation. (Ant)agonists of SXR are used to regulate metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              affinity receptor for reducing excessive levels of steroids in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel nuclear receptor polypeptide, designated SXR (steroid and xenoblotic receptor). SXR (i) forms a heterodimer with rethnoid X receptor (RXR). (ii) binds to a direct or inverted repeat response element motif based on the half-site AGTTCA, (iii) activates
                                                                                                                                                                                        involved in undesirable drug interactions. Antibodies specific for
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Sequence 2068 BP; 520 A; 541 C; 586 G; 420 T; 1 other:

Best Local Similarity

81.3%; 99.4%;

Score 1744.4; Pred. No. 0;

DH 20;

Length 2068

Ş D b В ç Ъ Qy P χ рb Ŷ Вb ŷ Дb Qy В Matches 1781; 481 gwatgcaagqgrittttcagqaagggccatgaaacgcaacqcccqqctqagqtqccccttc 640 460 400 760 361 580 520 121 aaqtqttcacaqtgayaaaaqcaaqaqaataagctaatactcctqtcctqaacaaqqcaq 301 241 cccaqqqqaqaaqtcqgaqcauaqaacttaccaccaaqcaqtccaaqaqqcccaqaaqcd 181 340 280 tgaaatataqqtgaqacaagattgtctcatatccggggaaatcataacctatqactaq 339 1 tgaaatataqqtqaqaqacaagattgtctcatatccggggaaatcataacctatqactaq atctuccqtqtatqtqqqqacaaqqccactqqctatcacttcaatqtcatqacatqtgaa aacctqqaqqtqaqacccaaaqaaagctggaaccatgctgactttgtacactqtqaqqac aagtqttcacaytgagaaaagcaagagaataagctaatactcctqtcctgaacaaqqcaq qacqqqaaqaggaagcactqcctttacttcaqtqqqaalctcqqcctcaqcctqcaaqcc gacqqqaayaygaaqcactgcctttacttcaqtqqqaatctcqqcctcaqcctqcaaqcc 120 acagagt.ctqttcctggaaagcccagtgtcaacgcaqatqaqqaaqtcqqqaqtccccaa aanntiggaggtgaganceaaaqaaagctggaaenatgetgactttgtanactgtqaggan cccaqqqqagaaqtcqqagcaaaqaacttaccaccaaqcaqtccaaqaqqcccaqaaqca acagaqtetqttcctggaaageeeagtgteaaegeagatqaqgaaqteqqaqqteeeaa cqqctccttqqtaaagctactccttgatcqatcctttqcaccqqattqttcaaaqtqqac atetgeeqtqtatgtggggaeaaggeeactggetateactteaatqteatqaeatqtqaa Conservative 0; Mismatches 7; Indels 3; Gaps 480 6,99 759 420 360 5.79 100 180 نيا ٠٠

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The specification describes a human intranuclear receptor protein The nucleic acid sequence was isolated from a human adult cDNA library using a swellfish ANO23 derived probe. The protein can be used for the development of drugs and diagnosis and treatment of various diseases. The present sequence was used in the course of the income diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NISB ) JAPAN TOBACCO
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                       gycatgaagaaggagatgatcatqtccgacgacgccqtqqaqqaqqaqqcqqqqccttqatc 678
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                                                                                                                                                                                                                               aggagqgccatgaaacgcaacgcccqqctgaggtgcccrttccgqaaqqqcqctqrqag
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99.48;
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Pred. No. 3.4e-148;
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                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A movel cDNA sequence encodes the rat vitamin D receptor isoform protein (VDRI). The isoform differs from the normal receptor (VDRI), which is encoded by the present sequence, in having the vitamin D response element curtailed by 86 residues, and having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extra 19 residues inserted at the C-terminal of this element. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding a vitamin D receptor isotorm protein - useful for density determination and for screening substances for vitamin
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1960 BP; 432 A; 620 C; 497 G; 411 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmission channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acts as a dominant negative receptor in the vitamin D signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 46pp; Japanese.
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(CHUS ) CHUGAI SELYAKU KK.
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                                                                                                                    PROCEEDINGS OF THE PROPERTY OF
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55.6%;
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                                                                                                                                                                                                                                      Score 278.8; 1
Pred. No. 1.6e
0; Mismatches
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RESULT 1
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AAU51425 standard; cDNA; 2043 BP

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                                                                                                                                                                                                                                                                                                 transformation of the insect host. The rat version of the coding sequence was published in Burmester et al., Proc.Natl. Acad.Sci 85;9499-9502 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant prodn. of 1,25-di:hydroxy-vitamin=D3 - using expression system comprising insect cell recombinant virus contg. foreign DNA
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                    gtacagogtaagaqqqaqatgataatqaagaqaaaaagaqgaaqaagqccttqaaggacagt
                               tgtgaaggatgcaagggctttttcaqqaggccatgaaacgccaacgcccggctgaggtgc
                                                           cggctcaaacgctgtgtggacatcggcatgatgaaggagttcatcctgacagatgaggag
                                                                      cycctycgcaagtgcctggagagcggcatgaagaaggagatgatcatgtccgacgaggcc
                                                                                                    cccttc---aatggagattgccgcatcaccaaggacaaccggcgacactgccaggcctgc
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Pred. No. 1.7e-62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity of the receptor may be detected by measuring changes in interactions with known collectors (e.g. SEC-1, GRIP-1 and TFILB) or unknown collectors (e.g. through use of the dual hybrid system). The polynucleotides shown in AAX34787, AAX34791 and AAX34792 (corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotides which encode novel isolorus of the human vitamin D receptor (VDR) or variant transcripts for LVDR. The polynucleotides are useful in methods for detecting agonist and /or antagonist compound of a VDR isolorus. An increase or decrease in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D receptor or variant transcripts for hVbR
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High-efficiency full-length cDNA cloning
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AW715492 RPCI-24-1
AW012320 um07d07.y
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                                                                                                                                                                                                                                                                                                          Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sasaki,D., Shibata,K., Shibata,Y., Shinaqawa,A., Shiraki, Soqabe,Y., Suzuki,H., Taqami,M., Taqawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y., Toya,T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was propared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                /db_xref="taxon:10090"
/db_xref="MGD:MGI:1337040"
/db_xref="MGD:MGI:1897757"
/tissue_type~"cecum"
/clone_lib="RIKEN_full-length_enriched_mouse_cDNA_library"
                                           /sex-"male"
                                                               /clone="9130016I18"
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                   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylic,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,H., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
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                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Entheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
L. (bases 1 to 794)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAGTGGCCCCCAGACAGTCTAGGACACACAGATGTAAACCTAGAGATGAGACCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aqaacttaccaaccaagcaqtccaagaggcccagaagcaaacctqgaggtgagacccaaag 322
                                                                                                                                          GGGCCATGAAACGCAATGTCCGGCTGAGGTGCCCCTTCCGCAAGGGAACCTGCGAGATCA
                                                                                                                                                                                                                                   AGGCCAATGGCTACCACTTCAATGTCATGACGTGTGAAGGATGCAAGGGGTTTTTCAGAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGCTGGAGCCGAGTTGGCCTTGTACAGTGTGAAGAAGCAGACTCTGCCTTGGAAGAGC
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: custom primer used High quality sequence stop: 472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (into a image. llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with an oligo(df) primer (ATGTGGCCTTTTTTTTTTTTTTTT);
double stranded cDNA was ligated to a DTAII adaptor (TGTTGGCCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer CGACCTGCAGCTCGAGCACA."

CGACCTGCAGCTCCAGCACA."

180 c 253 g 152 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pME18S-fL3; Site_1: DralII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage-"embryo, 14 dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Sugano mouse embryo mewa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone-"IMAGE:2<del>07</del>6282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain-"C57BL"
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79.3%;
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339 tgactttqtacactgtqaqqacacaqagtctgttcctqqaaaqcccaqtqtcaacqcaqa 98
                                                                                                                                                                           279 caqteeaaaqaqeeeagaagcaaacetggagqtgagaceeaaaqaaaqetqgaaceeatue 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 608 Std Erro
Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 608 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicqap
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 343)
                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructed by Bento Soares and M.Fatima Bonaldo."
108 c 93 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with rac I and cloned into the Pac I and Eco RI sites of the modified p1773 vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B (ampicillin resistant)"
/note-"Organ: Liver and Spieen; Vector: pT71xb (Pharmacia)
with a modified polylinker; Site_1: Pac 1; Site_2: Eco R1;
This is a subtracted version of the original Source fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib-"Soares_fetal_liver_spleen_lNFLS_Sl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1850687"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                             16.0%; ....
100.0%; Pred. No.
100.0%; Mismatches
                                                                                                                                                                                                                                                                                                         Score 343; DB 17; Pred. No. 3.7e-78; 0; Mismatches 0;
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                                                                                                          KOjima,Y., Konno,H., Konda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,k., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shidata,K., Shibata,Y., Shibadawa,A., Shiraki,T., Sopabe,Y., Suzuki,H., Taqami,M., Taqawa,A., Takahashi,F., Tanaka,T., Te)ima,Y., Toya,T., Yamumura,T., Yasunishi,A., Vosbida, Y., Toya,T., Yamumura,T., Yasunishi,A., Vosbida, Y., Toya,T., Yamumura,T., Yasunishi,A.,
                                                                                                                                                                                                                                                                                                                                                               Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanaqaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hoi,F., Inobani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kashiwaqi,K., Pujiwake,S., Inoue,K., Toqawa,Y., Izawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system - 884-format sequencing pipeline with 884 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Kikuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T.,
Harada,A., Yamamoto,R., Matsunoto,H., Sakaquchi,S., Ikeqami,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDMs to prepare tull-length cDM. libraries for rapid discovery of new connected to the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:2510047D01, tull insert sequence.
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                                                                                    Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection
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kiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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Best Local Similarity
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GGGCCATGAAACGCAATGTCCGGGTGAGGTGCCCCTTCCGCAAGGGAACCTGCGAGATCA
                                                                                                                         AGGCCAATGGCTAGCACTTGAATGTCATGACGTGTGAAGGATGCAAGGGGTTTTTCAGAA 494
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ANGVEENVMTCEGCKGFFRRAMKRNVKLKCPFRKGTGEITRKTKRQQQACKLKKCLES
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/clone_lib="RIKEN_full-length_enriched_mouse_cDNA_library"
/dev_stage="13_days_embryo"
105.__>677
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/db_xret="MGD:MG1:1894064"
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Local Similarity 97.7%;
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                                                                                                         Ctccttgatcgtttqcaccggattgttcaaagtqgaccccayqqqagaagtcggag
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                                          caaaqaacttaccaccaaqcaqtccaaqaggcccaqaagcaaacctqqaqqtqagaccca
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In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by
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AU099521 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSI07557 similar to Homo sapiens orphan nuclear receptor (PARL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki,ř., Yoshitomo-Nakágawa,Ř., Maruyama,Ř., Suyama,Ř. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library, Gene 200 (1-2), 149-156 (1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Jaj
Email: ysuzukijims.u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Virology
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/clone="HS107557"
/clone_lib="Sugano Homo sapiens cDNA library"
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Homo sapiens
Eukaryota; M
                                                                                                           N94132 454 bp mRNA EST 05-API za25q06.rl Soares tetal liver spleen lNFLS Homo sapious IMAGE:293626 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chinese National Human Genome Center at Shandhai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 201203, P. R. China Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV651714 638 bp mRNA EST 07-SEP-2000 AV651714 GLC Homo sapiens cDNA clone GLCCSG03 3', mRNA sequence AV651714
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This clone is available at CHGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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/tissue_type='corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host-"SOLR"
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 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Best Local Similarity
Matches 216; Conserv
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCTATGCCCACATACCCACGTTTGTTCGCTTCCTGAGTCTTTTCATTGCTACGTCTAA 126
                                                                                                                     AA277370 472 Bp mkNA EST 01-APR-1997 vabla12.rl Soares mouse NML Mus musculus cDNA clone IMAGE:737758 similar to Tk:G410518 G410518 ORPHAN NUCLEAR RECEPTOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Ritkin,L., Rohlting,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                     STEROID/THYROID SUPERFAMILY. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, No 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royally free through LLNL; confact the LMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wnstl.edu
                       house mouse
  Sulusculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone "imagk:29 025"
/clone_lib_"Sourés tetal liver spleen INFDS"
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/db_xref_"taxon: 9506"
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1696 geedaddadeedaatgeeet 1716
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Ouery Match 9.4%; Score 201; bH 4; Best Local Similarity 77.2%; Pred. No. 2.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1636
                                                                                                                                                                           1576 atgeagagitgiteggeateaeaggiagetgagetgeeettgagigaeaeereega 1635
                                                                                                                                                                                                                                                                      | 1456 qef cafaqqttettqttectqaaqateafqqcfatqcfcaccqaqctccqcaqcatcaat | 1515
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                                                                                                                                                                                                                                                                                                                                                               121 GCTCACAGGTTCCTGTTCCTGAAGATCATGGCCGTCCTCACTGAGCT GCGACATCAAC 178
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GGGCCAGCTAGACCCAGA -CATFCTGAATTGCCACTTCTAGGGCTAGACAGATGGACA-T
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                                                                                                                     A FGCAAGAGTTATTTAGCAGCACAGATGGCTGAGTTGCCCCCTGAGTGGAGAFCFCAT
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Contact: Marra M/Mouse EST Project
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Seq primer: -28ml+ rev2 ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
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130 AGGAACTTGCGGCTCAGCTGCCCCTTCCAGAA----TTCCTGCGTCATCAACAAGAGCAAT 186
                    514 cgcaangccnggctgaggtgcccnttbefgaagggcgcctgcgagatcannoggaagacc 573
                                                                                                           454 tatcacttcaatgtcatgacatgtgaaqgatgcaagggctttttcaggaqqqccatqaaa 513
                                                                                                                                                                                                            394 gcaqatqaggaagtcqqagytccccaaatctqccgtqtatqtqqqqacaaqqccactggc 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357
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                                                                                                                                                                      ACTGATAGCCAACAACGCCCT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Other ESTs: da94c06.xl
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 493)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW871811 493 bp mRNA EST 30-MAR-2001 da94c06.yl Xenopus laevis tadpole stage 24 Xenopus laevis cDNA 5' da94c06.yl Xenopus laevis tadpole stage 24 Xenopus laevis cDNA 5' conclusion to gb:J03258 VITAMIN D3 RECEPTOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R. MashU Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library constructed by B. Korn PhD. and S. Henze DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            through the RessourcenZentrumPrimarDatenbank, Berlin, Germany (web
address: www.rzpd.de)
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                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pcMVSPORT6; Site_1: NotI; Site_2: SalI; Method of cloning used: directed ligation; insertCheck: 95.8 blue and 4.2 white. Library constructed by Dr. Bernhard Korn and Sabine Henze: Note: This is a Xenopus
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/dev_stage="stage 24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: estawatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.qov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 154.
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Fax: 314 286 1810
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Holix Research Institute
1542-3 Yana, Kisarazu, Chiba
Tel: 81 438-52-3951
Fax: 81-448-52-3952
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His luman cDNA project; 5% & 3% end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
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Contact: Takao Isogai
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Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S.
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 Unpublished (1997)
Contact: Robert Strausberg, Ph
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                                                                                                                   Eukaryota; Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 215)

Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Eukuda,S., Fukuniashi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tatteno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yayame,M., Yamamura,T., Yokota,T., Yoshino,M., Okazaki,Y., and Hayashizaki,Y.
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                                         Unpublished (1999)
                                                                                        RIKEN Mouse ESTS
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/lab_host="DH10B"
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3-1-1 Koyadai, Tsukuba, 1baraki 305-0074, Japan
Email: cgapbs:r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1996). Transcriptional seguencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
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Thermostabilization and thermoschivation of thermolabile enzymes by
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                                                                                                                                                                          Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/dev_stage="l3-day embryo"
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Best Local Similarity 57.9%;
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High quality sequence stop: 668.
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                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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/db_xref:"taxon:10090"
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Best Local :
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                         775 cayatdaaacetttqaeactaeetteteecattteaaqaaftteeqqetqeea 828
                                                                                                463 CTGAG --GCCCAAGCTGTCTGAGTAGCAACAGCACATTATCGCCATCCTGCTAGATGCC
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                                                                                                                                                                                              403 GTGCAGCGTAAGCGAGAGATGATGAAGAGGAAGGAGGAAGAGGCCTTGAAGGACAGT 462
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                                                                                                                                                                                                                                                                                              34.3 COCCTCANACOCTGCGTGGACATTGGCATGATGAAGGAGTTCATCCTCACAGATGAGGAG. 4.02
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                                                                                                                                                                                                                                                                                                                                                                                                                                       cecttecqquaqqqqqctqcqaqateaccqqaaqacccqqcqacaqtqccaqqcctqc 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cqapbs r@mail.nih.qov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tound through the L.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUNA Library Preparation: Lite Technologies, Inc. cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLML) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Jettrey E. Green, M.D.
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/lab_host "bH10B (T1_phage=resistant)"
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/site_2: Sall; Cloned unidirectionally. Primer: Oligo d'
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RESULT 1 US-09-276-531-111 US-09-276-531-111 Sequence 111, Application Patent No. 6183/68 GENERAL INFORMATION: APPLICANT: Bandman, APPLICANT: Hillman, APPLICANT: Headyn, Henr APPLICANT: Reddy, Ro APPLICANT: Guegler, APPLICANT: Guegler, APPLICANT: Baudhn, M TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: STATE: CALIFORNIA COUNTRY: USA ZIP: 94304 COMPUTER READABLE FOR MEDIUM TYPE: FLOPP COMPUTER: ENCYTE SOFTWARE: Word Per CORPUTEN: APPLICATION UNDER: FILING DATE: March COLASSIFICATION UNDER: FILING DATE: March CLASSIFICATION TON TELECOMMUNICATION INF TELEPHONE: (650) 845 TELEFAN: (650) 845 TELEFANE: BOI DASE LENGTH: BOI DASE LENGTH: BOI DASE TYPE: nucleic acid TOPOLOGY: linear LIBRARY: SINTFETO3	28 80.8 29 80.8 30 79.6 31 79.6 32 79.6 33 77.6 34 74.8 36 74.8 37 74.4 40 74.4 40 74.4 41 73.2 42 73.2 68.6
an, Olga preceti an, Jennifer L. genry Roopa ar, Karl J. N. COMPOSITION FOR THE DETECTION OF GENES ENCOD N: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL ES: 134 PRECEPTORS AND PROTEINS ASSOCIATED WITH CELL ES: 134 PROPRIED PROPRIE	3.8 1860 2 US-08-372-652-7 Sequence 7, 3.8 1860 5 PCT-US95-16311-7 Sequence 7, 3.7 1659 1 US-08-333-358-7 Sequence 7, 3.7 1659 1 US-08-694-501-7 Sequence 7, 3.7 1659 1 US-08-694-501-7 Sequence 7, 3.6 1688 2 US-08-694-591-1 Sequence 7, 3.5 1649 2 US-08-469-6129-1 Sequence 1, 3.5 1649 5 US-08-469-6129-1 Sequence 1, 3.5 1649 5 US-08-4759-17 Sequence 1, 3.5 1649 5 US-08-144-759-17 Sequence 1, 3.5 1649 5 US-09-144-759-17 Sequence 1, 3.6 1688 1 US-09-144-759-21 Sequence 1, 3.7 2295 4 US-09-144-759-21 Sequence 1, 3.8 2468 1 US-08-4333-358-11 Sequence 1, 3.4 2468 1 US-08-463-694-501-11 Sequence 1, 3.4 2468 1 US-08-694-501-11 Sequence 1, 3.4 2468 1 US-08-694-501-11 Sequence 1, 3.4 2468 1 US-08-372-652-14 Sequence 1, 3.4 2468
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Rest Local Similarity 98.2%;
Matches 776; Conservative (
                                           Sequence 6, Application 05/077377368 Patent No. 5260199
       GENERAL INFORMATION:
APPLICANT: Delaca, Hector F
APPLICANT: Ross, Troy K.
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Pred. No. 6.7e-167;
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AUTHORS: Maeda, No. 52601, ...,
AUTHORS: Delica, heetor F.
AUTHORS: Delica, heetor F.
TITLE: Structure and regulation of the rat
TITLE: 1.25-dihydroxyvitamin D3 receptor
TOURNAL: Proc. Natl. Acad. Sci. U.S.A.
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INFORMATION FOR SEQ ID NO: 6:
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IELECOMMUNICATION INFORMATION:
TELEPHONE: 414-277-5715
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCHWALTE, CAIL R.
REGISTRATION NUMBER: 29,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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475
                                                                                                                                                                                                                                                         415 ecceaaatetgeegtstatgtggggaeaaggeeaetggetateaetteaatgteatgaea 479
                                                      332 GGGCTCAAACGCTGTGTGGACATCGGCATGATGAAGGAGTTCATCCTGACAGAGATGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 19910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IHM PC compatible OPERATING SYSTEM: PC:DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                     cqcctqcucaaqtqcrtqaaqaqcqqcatqaagaaqqadatqatcatqtccqacqaqqcc
                                                                                                                       CCCTTC - - - AATGGAGATTGCCGCATCACCAAGGACAACCGGGGACACTGCCAGGCCTGC
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                                                                                                                                                                                                                                                                                                                            629; Conservative
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1,25-bihydroxyvitamin D3 Receptor Protein
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                                                                                                                                                                                                                                                                                                                          0; Mismatches 482;
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Sequence 5, Application US/07737736B Patent No. 5260199
                                                                              GENERAL INFORMATION:
APPLICANT: DeLuca, Hector F.
APPLICANT: Ross, Troy K.
APPLICANT: Prahl, Jean M.
TITLE OF INVENTION: Method Of Producing
TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
                         CORRESPONDENCE ADDRESS: Carl R. Schwartz, Esq., c/o
                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 GTACAGCGTAAGAGGGAGATGATAATGAAGAGAAAAAGAGGAAGAGGCCTTGAAGGACAGT 451
                                                                                                                                                                                                                                                                                                                                                                                          ATGATCCAGAAACTGGCCGACCTGCGGAGCCTCAACGAGGAACACTCCAAAC 1280
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DATE: May-1988
US-07-737-736B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Schwartz, Carl R.
REGISTRATION NUMBER: 29.437
REFERENCE/DOCKET NUMBER: 96-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 414-277-5715
TELEFAX: 414-277-5774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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AUTHORS:
AUTHORS:
413 GTGCAGAGGAAGCGGGAGATGATCCTGAAGCGGAAGGAGGAGGAGGCCTTGAAGGACAGT
                                                                                                                                                                                               296
                                                                                                                                                                                                                                                                                                                                                                                          176 CCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTCACTTCAATGCTATGACC 2×
                                                                                             353 CGGCTCAAACGCTGTGTGGACATCGGCATGATGAAGGAGTTCATTCTGACAGATGAGGAA 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
AUTHORS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IF
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COUNTRY: U.S.A.
ZIP: 53202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE: Cloning and expression of full-length cDNA TITLE: encoding human vitamin D receptor JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
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                                                                                                                   eqeetqegcaagtqeetggaqageggeatgaaggaqgaqatqateatuteeqacuaqqee 651
                                                                                                                                                                                               CCCTTC - - - AACGGGGACTGCCGCATCACCAAGGACAACCGACGCCACTGCCAGGCTGC
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Pike, J. W.
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Crisp, Tracey M.
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INFORMATION FOR SEQ ID NO:
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REPERENCE/SECRET NUMBER: 00
TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 542-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MHDIUM TYPE: 4.5" Diskette,
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APPLICATION NUMBER: 07/843,350
FILING DATE: February 26, 1992
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Best Local s
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INFORMATION FOR SEQ ID NO: 1:
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TITLE OF INVENTION: CAR RECEPTORS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
1253 aacttetactgqagcccatgctgaaatteccactacatgctgaagaaqctqcaqctgcatg 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
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NAME: Paul T. Clark
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/843,350 FILING DATE: February 26, 1992
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STREET: 22
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                                                                                                                                                                                                                                                                                     CTCTGGTCACACACTTCGCAGACATCAACACTTTCATGGTACTGCAAGTCATCAAGTTTA 798
                                                          ACTTCCTCTGCGGGCCTCTTCGCTACACAATTGAAGATGCAGCCCGTGTGGGGGTTCCAGG
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; Patent No. 5756448
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                                                                                                US-07-843-350C-1
Query Match 7.9%;
Best Local Similarity 57.5%;
Matches 327; Conservative
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                                                                                                                                                                                                                TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
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MEDIUM TYPE: 3.5" Diskette,
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NAME: Paul I, Clark
REGISTRATION NUMBER: 30,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect (Version 5.0) CURRENT APPLICATION DATA:
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                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: February 26, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/843,3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
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                                                                                                                    TOPOLOGY:
                                                                                                                                                                        LENGTH: 1450
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IVENTION: CAR RECEPTORS AND RELATED

VENTION: MOLECULES AND METHODS
                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                30,162
Score 170.6; DB 1;
Pred. No. 7.7e-32;
0; Mismatches 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1219
                           REFERENCE/DOCKET NUMBER: 00786/126001 TELECOMMUNICATION INFORMATION:
                                                                                                                                                         FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.25.4
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                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: David D. Moore et al
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                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DoS (Version 6.80)
SOFTWARE: WordPailed (Version 5.0)
                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/843, 350
                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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TELEPHONE:
                                                                                                                                    NAM:::
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(617) 542-5070
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: Sequence 1. Application US/08342411A
; Patent No. 5639616
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                                                                                                                                                                                                                                                          TITLE OF INVENTION: UNIQUITOUS NUCLEAR RECEPTOR:
                                                                                                                                                                                                                                                                                                                            APPLICANT: LIAO, Shutsung APPLICANT: SONG, Ching
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                       STREET: F.
STREET: F.
STREET: WA
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COUNTRY: USA ZIF: 77210-4433

ADDRESSEE:

P.O. BOX 4433

Arnold, White & Durkee ъ В

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PCT-0893-01559-1
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INFORMATION FOR SEQ 10 NO: SEQUENCE CHARACTERISTICS:
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                                                       1553 tacaccectttgetaegececteatgeag 1581
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STRANDEDNESS: single
TOPOLICY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com

Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Polar-

PatentIn Release #1.0, Version

#1.30

CURRENT APPLICATION DATA:

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Hest Local Similarity 47.6%;
Matches 585; Conservation
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803 CAGCCCAAAGTCACGCCTGGCCCTGGGCGCAGACCCCCAGTCCCGAGATGCCCGCCAG
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STRANDEDNESS: single
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REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD154
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Pred. No. 2.2e-14;
0; Mismatches 569; Indels 76
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                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches,
MEDIUM TYPE: storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: Kalamazoo
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                                                               GENERAL INFORMATION:
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                              APPLICANT:
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APPLICATION NUMBER:
FILING DATE: 21 SEPT
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                                                                                                                                                                                          695 Jacqqacagggactcagccactgggagtgcag 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 329
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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STRANDEDNESS: double
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             Holloway, M. Katharine
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Schmidt, Azriel
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Best Local Similarity 54.8%;
Matches 215; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM
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TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
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695 aacqqacaqqqaetcaqccactgqqaqtqcaq 726
                                                                                          717 GCGTCCT FECTGAAGAACAGATCCGGAAGAAGAAGATTCGGAAACAGCAGCAGCAGGAGGT 776
                                                                                                                                                                                                                                                                                               575 qqqqacaqtqccaqqqcctqcqqcctqcqcaaqtqcctqqaqaqcqqcatqaaqaaqaya 634
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COMPUTER: IF
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Pred. No. 2.2e-14;
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RESULT 11 US-08-330-283-1

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NAME: DOLAN, CATHEFINE A.
REGISTRATION NUMBER: 36,502
REFERENCE/DOCKET NUMBER: 1932
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4283
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.5
Best Local Similarity 54.8
Matches 215; Conservative
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APPLICANT:
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ANTI-SENSE: 1
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MEDIUM TYPE: Floppy
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APPLICANT: Vogel, Robert
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                                                                                                                                                                          518 acgcccqqctqaqqtgccccttccqqaaggqcg---cctgcgagatcaccccqqaaqaccc 574
                                                                                                                                                                                                                                                                                                                                  398 atgaggaagtcggaggtccccaaatctgccgtgtatgtygggacaaggccactggctatc 457
717 GCGTCCTTTCTGAAGAACAGATCCGGAAGAAGAAGATTCGGAAACAGCAGCAGCAGGAGT 776
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                                635 tgatcatgtregaeyaggeeqtqqaggaggaggeecttqateaaqeggaagaaaagtg 694
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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126 East Lincoln Avenue
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54.8%;
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Pred. No. 2.2e-14;
0; Mismatches 174; Indels
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US-08-646-248-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1,
                                                                                                                                                                                                                                       Query Match 4.5%;
Best Local Similarity 54.8%;
                                                                                                                                                                                                                         Matches 215;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: HAM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
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APPLICANT: Schwidt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: DOLAD, Catherine A.
REGISTRATION NUMBER: 36,502
REFERENCE/DOCKET NUMBER: 19-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/330,283
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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CITY: 1
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STRANDEDNESS: single
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                                                                       CCCCGAAGATGCTGGGCCACGAGCTTTGCCGTGTGTGTGGGGACAAGGCCTCCGGCTTCC
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PCT 0895 13924 1
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Best Local Similarity 54.8%; Pred. No. 2.2e 14;
515. Conservative 0; Mismatches 174; Indels
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TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
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                                                                            417 CACACTEGGECATCCCAGATECCGAAGAGGAAGCAAACCAGAGCGCAAACGAAAGAAGGGCCCAG 476
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OPERATING_SYSTEM: PC-DOS/MS_DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2030 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAM::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEGERETTTETGAAGAACAGATCGGGAAGAAGAAGAFFEGGAAACAGCAGCAGCAGCAGT 776
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Ouagliate, Carol S.
114
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Schmidt, Azriel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Friedman, Eitan
Holloway, M. Katharino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rodan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (908) 594-3809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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                                                                                                                                                                                                                                                                                                 Score 97.6: DB 5: Length 2030;
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PCT-US95-13931-1

Sequence 1. Application PC/TUS9513931

GENERAL INFORMATION:
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Query Match 4.5%; Score 97.6; DB 5; Length 2030; Best Local Similarity 54.8%; Pred. No. 2.2e-14; Matches 215; Conservative 0; Mismatches 174; Indels v
                                                                                                                                                                                                                                                                                                   TELEFAX: (908) 594-47
INFORMATION FOR SEQ ID NO:
                                                                                                                                              MOLECULE TABLE NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version CURRENI APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALIABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LHM PT compatible
OPERATING SYSTEM: PC-UDS/MS DOS
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APPLICANT: Holloway, M. Ka
APPLICANT: Kodan, Gideon
                                                                                                                              ANTI-SENSE: NO
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                     NAME: Quagliato, Carol S.
REGISTRATION NUMBER: 35,330
REFERENCE/DECKET NUMBER: 19316 PCT
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                                                                                                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                       TYPE:
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                                                                                                                                                                                          Linear
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                                                                                                                                                                                                                                                                                                                                             (908) 594-3809
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                                                                                                                                                                      DNA (genomic)
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                                                                             REFERENCE/DOCKET NUMBER: ARC
TELLCOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEFAX: (713) 789-2679
TELEFAX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: BARBARA S. KITCHELL
REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,003
FILING DATE: 10-NOV-1993
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: 1
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: Concus
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCI1
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: #1.25
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            LENGTH: 1813 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Arnold, White & Durkee P.O. Box 4433
                                            1813 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
linear
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                                                                                                                                                                             33,928
                                                                                                                                                                 ARCD154P--
                                                                                                                                                                                                                                                                                                                                                                                    Version
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Search completed: July 11, 2001, 16:30:20 Job time: 14255 sec

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OM protein - protein search, using sw model
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 THB1_HOMAN
THB_RANCA
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THB2_HOMAN
THBB_XENLA
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THB_PAROL
ECR_LUCCU
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17.9 606 1 E75_METEN	391 17.9 418 1 THAB_XENLA	393 18.0 418 1 THA_RANCA	394 18.0 410 1 THA1_SHEEP	. 397.5 18.2 402 1 THA_PYGAD	397.5 18.2 402 1 THA_APTPA	401.5 18.4 408 1 THA_CHICK	38 402.5 18.4 556 1 ECR_MANSE	406 18.6 416 1 THAA_PAROL	411.5 18.8 536 1 ECR_CHITE	411.5 18.8 427 1 THA1_BRARE	18.9 514 1 THB2_RAT
077245 metapenaeus	P18115 xenopus lae	Q02777 rana catesb	Q28570 ovis aries	042450 pygoscelis	042295 aptenodytes	P04625 gallus gall	P49883 manduca sex	Q91241 paralichthy	P49882 Chironomus	098867 brachydanio	P37826 rattus norv

ALI CNMENTS

		RESULT PXR_HU ID F AC C
This SWISS-PROT between the Swi the European Bio use by non-promodified and thi entities require or send an email EMBL, AP084645; MIM; 603065; InterPro; 1PR000	15 JUL-1999 (No.). 16 JUL-1999 (No.). 10 L-OCT-2000 (Rel. 4 ORPHAN NUCLEAR RECE RECEPTOR PARI) NRI12 OR PXR. HOMO SAPIERS (HUMAN ELIKARYOTA; Metazod; MAMMABIA 13; Eutheria: NCBI_TAXID-9606; SEQUENCE FROM N.A. TISSUE=Liver; MEDLINE-98395173; FLEHMAN FROM N.A. TISSUE=Liver; The human orphan n regulates CYP3A4 96 J. Clin. Invest. 10; SEQUENCE FROM N.A. TISSUE=Liver; MEDLINE-9844550; FBETTISSUE=Liver; MEDLINE-9846550; FBETTISSUE-10 (PPARE) BETTISSUE-11 (PPARE) FRENKANE BINDS -1- SUBGUNIT: FORMS -1- TISSUE SPECIFIC INTESTINE1- INDUCTION: ACTI PRECAMENICAE -1- TISSUE SPECIFIC -1- INTESTINE1- SUMILIARITY: BEI	1 MAN XR_HUMAN 375469;
entry is co ss Institut informatics fit instit s statement s a license to license hAAD05436.1; AAC64558.1;	15-JUL-1999 (Re). 48, Last Sequence update) 01-OCT-2000 (Re). 40, Last annotation update) 01-OCT-2000 (Re). 40, Last annotation update) 0RPHAN NUCLEAR RECEPTOR PXR (PRECNAME X RECEPTOR) RECEPTOR PARI). RECEPTOR PARI). RATIZ OR PXR. HOMO Sapiens (Human). EUKARYOTA: Metazoa; Chordata; Craniata: Vertebrata; Rammalia; Eutheria; Primates; Catarrhini; Hominidae NCBL_TaxID-9606; SEQUENCE FROM N.A. IISSUE=Liver; MEDLINE-98395173; PubMed-9727070; Lebmann J.M., McKee D.D., Watson M.A., Willson T.M. Kliwer S.A.; **The human orphan nuclear receptor FXR is activated "The human orphan nuclear receptor FXR is activated "The human orphan nuclear receptor for resulting int J. Clin. Invest. 102:1016-1023(1998). [2] **EQUENCE FROM N.A.** **TISSUE=Liver; **MEDLINE-98445350; PubMed-9770465; **BEDLINE-98445350; PubMed-9770465; **BEDLINE-983517; PubMed-9770465; **BEDLINE-983517; PubMed-9770465; **BEDLINE-983517; PubMed-9770465; *	⇒ ×
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InterPro: 1PR001628;
                                                                                                                                                                  15-JDE-1999 (Ref. 38, Created)
15 JUL 1999 (Ref. 38, Last sequence update)
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                                                                            Bukaryola: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi:
Mammalia: Butheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus
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MEDLINE 98149345; PubMed-9489701;
              CISSUE Liver.
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"An orphan nuclear receptor activated by pregnancs defines a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kliewer S.A., Moore J.T., Wade L., Standinger J.L., Watson M.A.,
Jones S.A., McKee D.D., Oliver B.B., Willson T.M., Zetterstrom F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRECIMANE: BINDS TO A RESPONSE ELEMENT IN CYPTA GENES PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 92:73-82(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                steroid signaling pathway.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS: PRO0047: STROIDFINGER.
PRINTS: PRO0446: STRDHOMBONER.
PRINTS: PRO0446: STRDHOMBONER.
PRINTS: PS00031: NUCLEAR_RECEPTOR: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00104; hormone_rec; 1.
Pfam: PF00105; z1-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIAMORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SN FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZN FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zine-timeer: Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPK001628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1837040; Nr112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONTH-PNC
240 LADVSTYMEKGVINFAKVISYERDLPTEDQISLLKGATEEMCILRENIMEDTETGTWECG
                                         243 MADMSTYMERGIISEAKVISYERDLPIEDGISLLKGAAFELGGLRENTVENAETGIWEGG 402
                                                                                        180 ELPEFLOASLLEDPATWSQIMKDKVPMKISLQLKGEDGSIWNYQPPSKSDGKELIPLLPH 239
                                                                                                                               183 ELPESIÇAPSREEAAKWSQVRKDLCSLKYSIQLRGEDØSVWNYKPPADSJGKETFSILPH 242
                                                                                                                                                                              120 ALIKEKKREKTEAPPPGGQGUTEEQQALIQELMBAQMQTFDTTFSHFKDFKLPAVFHSGC 179
                                                                                                                                                                                                                        123 ALIKEKKSEKTOTOPLGVOGLTEEOKMMIRELMDAQMKTFDTTESHFKNFKLPGVLSSOC 182
                                                                                                                                                                                                                                                                    60 GEFERAMKENVELIGPERKGTGELTEKTEROGQAGKLEKGLESGMKKEMIMSDAAVEQER 119
                                                                                                                                                                                                                                                                                                              63 GEFRRAMKRNARLEGPERKGAGEITRKTRROGOACRLEKGLESGMKKEMIMSDEAVEERR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: FORMS A HETERODIMER WITH WAR.
SUBGUNIT: FORMS A HETERODIMER WITH WAR.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PAR.1 (SHOWN HERE) AND
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PAR.1 (SHOWN HERE) AND
ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1/PAR.1 (SHOWN HERE) AND
PREGNENOLORE AND PROGESTERORE, SYNTHETIC CHUCKOCH COLDS AND
PREGNENOLORE AND PROGESTERORE, SYNTHETIC CHUCKOCH COLDS
AND
                                                                                                                                                                                                                                                                                                                                                            1 MRPEESWSRAGIAOCEEADSALEEF-INAEEEDOOLOICRACODKANGYHENAMICEGCK 59
                                                                                                                                                                                                                                                                                                                                                                                                    3 VRPKESWNHADEVHCEDTESVPGKPSVNADEEVGGPQJCRVCGDKATGYHFNVMICEGCK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTIGLOCOGORFICOIDS AND 16-ALPHA-CARHONITRILE (PCN).
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NR1 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF031814; AAC39964.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108000536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1PR000324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 11 AA;
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38
74
105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49567 MW;
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2.5
2.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGAND-BINDING.
MISSING (IN ISOFORM 2).
; F592AF91F689329E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4 TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HINGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR KECEPTOR TYPE
                                                                                                                                                                                                                                                                                                53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Gaps
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Query Match
Best Local Similarity
                                                                                                                                                             Pfam; PF00104; hormone_rec; 1.
Pram; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR
PRINTS; PR00398; STRDHORMONER.
PROSITE; PS00031; NUCLEAR_RECEEPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PXR_RAT O9R1A7;
                                                                                           DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
0RPHAN NUCLEAR RECEPTOR PXR (PREGNANE X RECEPTOR).
                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arch.
                                                                                                                                                                                                                                                                                                  EMBL; AF151377; AAD47214.1; -.
                                                                                                                                                                                                                                                                                                                           or send an email to licensewisb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99345883; PubMed=10415106;
Zhang H., LeCulyse E., Liu L., Hu M., Matoney L., Zhu W., Yan B.;
"Rat pregnane X receptor: molecular cloning, tissue distribution,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NR112 OR PXR
                                                       SEQUENCE
                                                                                                                                   Zinc-finger
                                                                                                                                                Receptor;
                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xenobiotic regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420
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63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303
                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: FORMS A HETERODIMER WITH RXR (BY SIMILARITY) SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: ORPHAN RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             نب
                                                                                                                                                                                                                                                                                                                                                                                                                                       NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREGNANE, BINDS TO A RESPONSE ELEMENT
                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLMQELFGIT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLMQELFSST 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOLQERFALTLKAYIECSRPYPAHRFLFLKIMAVLTELRSINAQQTQQLLRIQDSHPFAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLAYCFEDPNGGFQKLLLLDPLMKFHCMLKKLQLHKEEYVLMQA1SLFSPDRPGVVQRSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   norvegicus (Rat).
                                                                                                                                                                                                                                            IPR001628; - IPR001723; -
                                                                                                                                                Transcription
                                                                                                                                                                                                                                                                                   IPR000324;
                                                                                                                                                                                                                                                                        IPR000536;
                                                  38
38
74
105
202
431
                                                       A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                         NUCLEAR_RECEPTOR; 1. iption regulation; DNA-binding; Nuclear protein;
                                                     49660
75.7%;
72.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368:14-22(1999).
CEPTOR; ITS NATURAL LIGAND IS
                                                       ME.
Score
Pred.
                                                                  HINGE.
LIGAND-BINDING
                                                                                          NUCLEAR RECEPTOR-TYPE C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crahiata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi;
                                                       4B545F21F9439697 CRC64;
1656.5; DB 1
No. 4.9e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431
                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IN CYP3A
              DB 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                           and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENES PROMOTER
              Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FAT 402
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VDR_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      013124;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
                                                   This
                                                                                                                                                                                                                                                                                                                                     Endocrinology 138:2347-2353(1997).
-I- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3
-THE EXPRESSION OF HORMONE SENSITIVE GENES.
-I- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97307679; PubMed-9165021;
Li Y.C., Bergwitz C., Jueppner H., Demay M.B.;
"Cloning and characterization of the vitamin D receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDR OR NR111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDR_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae;
                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                              laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403 PLMOELFGIT 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 LADVSTYMEKGVINEAKVISHERELPIEDQISLLKGATFEMCILKENIMEDTETGTWECG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMRE outstation. European Bioinformatics Institute. There are no restrictions on its
                                                                                                                              DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL IN
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING INMAIN
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                  TISSUE SPECIFICITY: DETECTED IN ALL THE TISSUE EXAMINED. HIGHEST LEVEL N SMALL INTESTINE AND SKIN.
DEVELOPMENTAL STAGE: FIRST DETECTED AT STAGE 13. INCREASES GRADUALLY AND PEAKS AT STAGE 57-61 THEN DECREASES TO THE LEVEL
                                                                                                                                                                                                               SEEN IN ADULT
                                                                                                        NR1 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSFDRPGVLQHRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MADMSTYMEKGIISEAKVISYERDLPIEDQISLIKGAAFELOQIRENTVENAEIGTWEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESUMKKEMIMSDEAVEERR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQICKVCGDKATGYHFNVMTCEGCK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLMOELFSST 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQLQERFALTLKAYIECSRPYPAHRFLFLKIMAVLTELRSINAQQTQQLLRIQDIHPFAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQLQEQFA1TLKSY16CNRPQPAHRFLFLKIMAMLTE:
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Best Local
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                                                                                                             01-FEB 1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
40-MAY-2000 (Rel. 39, Last amonation update)
VITAMIN D3 RECEPTOR (VDR) (1,25 DIHYDROXYVITAMIN D3 RECEPTOR).
                                                         Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Gallitormes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plum; PF00104; hormone_rec; l. Plum; PF00105; zf-C4; l.
SEQUENCE FROM N.A
                                                                                                                                                                                                 VDR COTJA
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                              NCBI TaxID 93934;
                                                                                                        VIDE OF NEITL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) ARE PRODUCED BY USE OF
ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA-HINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
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PRINTS: PRO0(50; VITAMINDR.
PROSITE; PS000(8); NUCLEAR_RECEPTOR; 1.
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Pfam; PF00105; 21.C4; 1.
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or send an email to license#isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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"The avian vitamin D receptors: primary structures and their
origins":
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                                                                                 247 MLPHLADLYSYSTOKYTGFAKMTEGERDLTAEDQTALLKSSATEVIMLKSNQSFIMEDMS
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                                                                                                                                                                  LLPHMADMSTYMEKGIISFAKVISYFROLPIEDQISLLKGAAFEL/QLKFNTVFNAETGT
                                                                                                                                                                                                                                                   SQDFSSEDSNUVFGSDAFGAFPEPMEPQMFSNLDLSEESDESPSMNLELPH------LP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMETORE SOUCKTIKDNERHOOACELKECVDIGMMKEFILTDEEVQEKEEMILKEKEEE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARLEGFERKGAGELTEKTERQGQAGELEKGLESGMKKEMIMSDEAVEEERALIKEKKSEE 132
                                                                                                                                                                                                                                                                                                                                     SSCCELPESIQAPSREEAAKWSQVRKDLCSLKVSLQLKGEDGSVWNYKPPADSGGKELFS
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38.8%; Pred. No. 1.
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8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VITAMIN D3 RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LICAND-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97223369; pubMed<p056239;
Lu Z., Hanson K., Deluca H.F.;
"Cloning and origin of the two forms of chicken vitamin D receptor.";
Arch. Biochem. Biophys. 339:99-106(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      042392;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UIL-1999 (Rel. 38, Last annotation update)
VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
VDR OR NRIII.
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of sicinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use of the property institutions as long as its content is in no way use the property institutions as long as its content is in no way
                                                                                            Pfam: PF00104; hormone_rec; Pfam: PF00105; zf-C4; 1.
                                                                                                                                                          EMBL; AF011356; AAB62579.1;
                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                for vitamin D.";
Science 235:1214-1217(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                           McDonnell D.P., Mangelsdorf D.J., Pike J.W., Haussler M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-LEGHORN; TISSUE-Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
INIT_MET
              CHAIN
                        CHAIN
                                    Zinc-finger.
                                                        PRINTS; PR00350; VITAMINDR.
PROSITE; PS00031; NUCLEAR_RECEPTOR:
                                                                                 PRINTS; PR00047; STROIDFINGER
                                                                                                                                                                                                      modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                   O'Malley B.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87149040; PubMed=3029866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 45-114 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDR_CHICK
                                               Receptor; Transcription
                                                                                                                      InterPro;
                                                                                                                                 InterPro; IPR000536;
                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular cloning of complementary DNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427
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                                                                                                                                                                                                                                                                                    ALTERNATIVE INITIATION CODONS.

TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND INTESTINE.

TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND INTESTINE.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.

A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) ARE PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3
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                                                                                                                                                                                                                                                                            SUBFAMILY.
                                                                                                                     IPR001628;
                                                                                                                                           IPR000324; -.
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15
                                            regulation; DNA-binding; Nuclear protein;
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           VITAMIN D3 RECEPTOR, VITAMIN D3 RECEPTOR,
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  FORM B
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Best Local
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ZN_FING
Proc.
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DOMAIN
                     CDNA.
                                                                    SEQUENCE OF 58-423 FROM N.A
                                                                                                       receptor
                                                                                                                               MEDLINE: 89071726; PubMed=2849110;
Burmester J.K., Wiese R.J., Maeda
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                            NCB1_TaxID=10116;
                                                                                                                                                                                                                Rattus norvegious (Rat).
                                                                                                                                                                                                                                                                         P13053;
01-JAN-1990
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                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                            VDR OR NR111
                                                                                                                                                                                                                                                                                                 VDR_RAT
                                                                                                                  "Structure and regulation of the
                                                                                                                                                                                                                                                                                                                                                           415
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                                                                                                                  Maeda N.,
f the rat
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MEDLINE 88124963: PubMed-2829212;
Burmester J.K., Maeda N., Deluca H.F.;
"Isolation and expression of rat 1,25-dihydroxyvitamin D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN DR BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLLMAICILSPORPGVQDTSLVESIQDRLSDILQTYIRCHPPPGSRLLYAKMIQKLADL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMLRSNQSFTMEDMSWTCGSNDFKYKVSDVTQAGHSMDLLEPLVKFQVGLKKLNLHEEEEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 1.6e-54:
1: Mismatches 148
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                                85:1005-1009(1988)
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                                                                                                                                                                                                                                                    85:9499-9502(1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2078B6A6C8D8E5FC
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                                                                                                                                                                                                                                                                                                                                           Deluca H.
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   CONTROLLING
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Hest Local Similarity
Matches 164; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for some ontitles requires a license some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00104; hormone_rec; I. Plam; PF00105; zf-c4; I. PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc tinger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPROU0536;
InterPro: IPROU1628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A31367; A31367
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or send an email to licensewish sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PSO0031; NUCLEAR_RECEPTOR: 1.
Receptor: Transcription regulation; DNA binding: Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS: PRO0350; VITAMINDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro:
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                                                                                                                                                                                                                                                                                                                                                                                                                      88 POTCKVCGDKATGYHENVMTCEGYKGFFKKAMKRNAKLRCYERKGACETTRKTEROCQAC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBGRELULAR LOCATION: NUCLEAR.

BYMAIN: COMPOSED OF THREE DOMAINS: A MODILATING N-TERMINAL DOMAIN.
A DAMA-HINDING DOMAIN AND A C-TERMINAL STEROID-HINDING DOMAIN.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRT SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE EXPRESSION OF HORMONE SENSITIVE GENES
                                 PAHRELELK I MAMLTEE
                                                                                                                                                                                                    PSGESNIDLNGEDSD · ·
                                                                                                                                                                                                                                                                                                   QMKTEDTTESHEKNERLEGYL -SSGCELPESLQADSKEEAAKWSQVRKDLCSLKV----
                                                                                                LKEHYMLKKIQLHEEEYVLMQATSLESPDRPGVLQHRVVDQLQEQFATTLKSYTECNRPQ
PGSHQLYAKMIQKEADLESENEEHSKQYRSESEQFENSMKEFPEVEEVFG 419
                                                               TREQUELKKI,NLHEEEHVIJMATCTASPERPGVQDAKI,VEATQDRISNTLQTYTRCHIPP 369
                                                                                                                                 LTSDD01VLLKSSA1EV1MLRSNQSFTMDDMSWD0GSQDYKYDVTDVSKAGHTLEL1EPL
                                                                                                                                                               LPTEDQTSILKGAAFELCQLRENTVFNAETGTWECGKLSYCLEDT - - - AGGEQQLLLEPM
                                                                                                                                                                                                                                                                   HHKTYDPTYADERDERREVERMIOSTGSYSER----PELSESONSSSSSSDLYTTSLIMME 194
                                                                                                                                                                                                                                                                                                                                    RESERVED FORMAKEETEETTEEVQRKREMENKRKEEEEALKDSERPK ESEEQQHEEAILEDA 188
                                                                                                                                                                                                                                                                                                                                                                   RERECTESOMEKEMIMSDEAVEERRALIKKEKESERTOTOPLGVQGETESORMMIRELMDA 157
                                                                                                                                                                                                                                                                                                                                                                                                   PRICGVCGDRATGFHENAMTCEGCKGFFRKSMKRKALFTCPF-NGDCRITKDNRRHCQAC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P0+472; 1HCQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JU4147; AAA41089.1;
                                                                                                                                                                                                                                  -SLQLKGEDSSVWNYKPPADSGGKETESLLPHMADMSTYMFKGT1SFAKVISYFKD-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPR000324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 762; DB 1;
Pred. No. 4.5e-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGAND BINDING.
1A0E519A9DCCE990 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 128;
                             ATPIMORIFG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 423;
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Best Local
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The consequent middle contact that is not removed. Usage by and for common modified and this statement is not removed. Usage by and for common entities constant as a content is a content of the common continues.
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dene 152:281-282(1995)
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THE EXPRESSION OF BORMONE SENSITIVE GENES.

THE EXPRESSION OF BORMONE SENSITIVE GENES.

THE SUBGELLULAR LOCATION: NUCLEAR BORDONE OF THERE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN,
THE SUBJECT OF THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                             ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zinc-tinder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ptam: PF00104: hormone_rec; 1.
Ptam: PF00105: z1-C4; 1.
PKINTS: PK00047: STKOIDFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:103076; Vdr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to licensewish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE 95137405; PabMed 7835717;
Kamei Y., Kawada T., Fukuwatari T., Ono T., Kato S., Suqimoto E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia: Sciuroquathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                  ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNIH VNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor: Transcription regulation: DNA binding: Nuclear protein:
Zinc-tinger: Phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS: PRO0450: VITAMINDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR000536;
InterPro: IPR001628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: D31969; BAA06737.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and sequencing of the gene encoding the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_Tax1D 10090;
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                201 OVRKDLOSLKVSLQLRGEI/GSVWNYKPPADSGGKETFSLLPHMADMSTYMFKGTISFAKV
                                                                                     158 OMKTEDTTESHEKNERLD - GVLSSGCELD - - - - - - ESLOADSKE - EAAKWS
                                                                                                                                                                                                21 PRICGYCGDRATGEHENAMTGEGCKGFERRSMKRKALFTCPF NGFCRITKDNRRHCQAC 79
                                                                                                                                                                                                                                38 PQTORVOGDKATGYHENVMTOEGOKGFERRAMKRNARLKOPERKGACEITKKTRKQCQAC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NET SUBFAMILY.
                                                    HHKTYDPTYADFRDFRPP1RADVSTGSYSPRPTLSFSGDSSSNSDLYTPSLDMMEPASFS
                                                                                                                                                          RERKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIKELMDA 157
                                                                                                                       RLKROVDIGMMKEFILTDEEVQRKREMIMKRKEEEALKDSLRPK-LSEEQOHIIAILLDA
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39,98)
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                                                                                                                                                                                                                                                                   69; Mismatches 120; Indels 61; Gaps
                                                                                                                                                                                                                                                                                    Pred. No. 2.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                             C4-TYPE.
                                                                                                                                                                                                                                                                                                   Score 753.5;
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|; | 4704008172445732 | CR064
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DH 1;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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"Nucleotide sequence of the bovine vitamin D3 receptor.";
"Nucleotide sequence of the bovine vitamin D3 receptor.";
J. Dairy Sci. 79:1313-1315(1996).
-i- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
                                                                                                                                                                                                                                                                                                                                  PROSITE: PS00031: NUCLEAR_RECEPTOR: 1. Receptor: Transcription regulation; DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zi-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U50200; AAB01543.1; HSSP; P03372; LHCQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
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                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS: PR00047; STROIDFINGER. PRINTS: PR00350; VITAMINDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97034797; PubMed=8880453;
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SUBCELLULAR LOCATION: NUCLEAR.
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A DNA-HINDING DOMAIN AND A C-TERMINAL STERCID-BINDING DOMAIN
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
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[5]
                                                                                                           Miyamoto K., Kesterson R.A., Yamamoto H., Taketani Y.,
Tatsumi S., Inoue Y., Morita K., Takeda E., Pike J.W.;
"Structural organization of the human vitamin D recept
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-97355582; PubMed-9212063;
                                                                                                                                                                                                                                                                                                                                                                                                                          Rae
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                                                                                      and its promoter."
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                                           Endocrinol.
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M.R., Pike J.W., Shine J., O'Malley B.W
                                                                                                                                                                                                                                                                                                                                                                          (SEP-1997) to the EMBL/GenBank/DDBJ databases
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                                           11:1165-1179(1997).
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J. Clin.
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Some F., Marx S.J., Liberman U.A., Pike J.W.;
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gene confers hereditary resistance to 1,25-dihydroxyvitamin D3.";
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"A novel mutation in the deoxyribanucleic acid-binding domain of the
vitamin D receptor causes hereditary 1,25 dibydroxyvitamin D resistant
                                                                                                                                                                                                                                                            basis of steroid hormone receptor DNA-binding domain crystal structures.";
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strand conformation polymorphism analysis for heterozygous carrier
detection. *;
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"A unique mutation in the vitamin D receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor gene in three "A unique mutation in the vitamin to receptor general and the vi
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                                                                                                                                                                                                                                                                                                                      *Two mutations causing vitamin b resistant rickets:
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"Hereditary 1 alpha,25-dihydroxyvitamin b-resistant rickets resulting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Invest.
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Endocrinol.
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81:2564 2569(1996)
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DNA_BIND
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ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dnd
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InterPro: IPRO00536: -.
InterPro: IPRO01628: -.
Ptam: PRO01634: '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dihydroxyvitamin D(3): point mutations confer reduced transactivation in response to ligand and impaired interaction with the retinoid X receptor heterodimeric partner."
Mol. Endocrinol. 10:1617-1631(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS SER 414 AND CYS-49].
Whither 97320500; PubMed-8961271;
Whithield G.K., Selzoick S.H., Haussler C.A.
Galligan M.A., Jurutka P.W., Thompson P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 601769;
MIM; 277440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP
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"Vitamin D receptors from patients with resistance to
                                                                                                                      Zinc-tinger;
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                                                                                                                                                  Receptor: Transcription regulation; DNA-binding; Nuclear protein:
                                                                                                                                                                                 PROSITE: PSUGUAL:
                                                                                                                                                                                                          PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE LITTURE WAY PROJUCTED THE ACTION OF VITAMIN D3 BY CONTROLLING THE LITTURE GENES.

SIDE ELUTIAN TO OF THREE DOMAINS: A MODILATING N'TERMINAL DOMAIN, DOMAIN: COMPOSED OF THREE DOMAINS: A MODILATING N'TERMINAL DOMAIN, A DINA BLUNDING DOMAIN AND A C'TERMINAL STEROID-BLUNDING DOMAIN. OF REGISTER OF THE LITTURE (ALSO DISEASE: DEFECTS IN VDR ARE THE CAUSE OF TYPE LIA RICKETS (ALSO KNOWN AS HYPOCALCEMIC VITAMIN D'HESISTANT RICKETS (HUDRE)). HYDRE IS MOST FREQUENTLY AN AUTOSOMAL RECESSIVE DISEABLE CHARACTERIZED BY SEVERE RICKETS, HYPOCALCEMIA AND SECONDARY HYPOCALCEMIA SOLUTION AND SECONDARY HYPOCALCEMIA SECONDARY HYPOCALCEMIA SOLUTION AND SECONDARY HYPOCALCEMIA SOLUTION AND
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Clin. Invest. 99:297-304(1997)
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AH002164; HAAB3389;
AH002165; HAAB3389;
AH002165; HAAB3389;
AH002167; HAAB3389;
                                                                                                                                                                                                                                                                     PF00104: hormone_rec; 1. PF00105: zf C4: 1.
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2: IHCQ.
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S24174
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NUCLEAR RECEPTOR-TYPE
C4-TYPE.
C4-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions on nq as its content is in no
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for hormone
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ORPHAN NUCLEAR RECEPTOR NRII3 (CONSTITUTIVE ANDROSTANE RECEPTOR) (CAR)
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                             TISSUE-Liver;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Baes M., Gulick T., Choi H.S., Martinoli M.G., Simha D., Moore D.D.;
"A new orphan member of the nuclear hormone receptor superfamily that
interacts with a subset of retinoic acid response elements.";
Mol. Cell. Biol. 14:1544-1552(1994)
-i- FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RESPONSE
ELEMENTS THAT CONTROL EXPRESSION OF THE RETINOIC ACID RECEPTOR
BETA 2 AND ALCOHOL DEHYDROGENASE 3 GENES.
                                                                                                                                                                                  MEDLINE=94158827; PubMed=8114692;
                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                        (ORPHAN NUCLEAR RECEPTOR MB67).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      + + + +
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TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
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Similarity 40.5%; Pred. No. 1.1e-51
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NRI3_RAT Q9QUS1; 01-0CT-2000 01-0CT-2000

STANDARD;

PRT;

(Rel. 40, Created)
(Rel. 40, Last sequence

RAT

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sexually dimorphic nuclear translocation of receptor CAR and induction of cyp281 grow by phenobalbital in rat livers."; Submitted (MAK 1993) to the EMBLYCOMBAN ZUBAL databases.

1. FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RESPONSE ELEMENTS. THAT CONTROL EXPRESSION OF THE RETINOIC ACID RECEPTOR HETA 2 AND ALCOHOL DEHYDROGENASE 4 GENES (BY SIMILARITY).

1. SUBGULLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plan; PE00104; hormone rec; 1.
Plan; PE00105; zf C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0350; VITAMINDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi:
Mammalia: Eutheria: Rodentia: Scinroquathi: Muridae: Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                              21110
                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00031; NUCLEAR RECEPTOR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interprop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yoshinari K., Sueyoshi T., Moore R., Neqishi M.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN WISTAR KYOTO, AND FISCHER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCBI TaxID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORPHAN NUCLEAR RECEPTOR NRITH (CONSTITUTIVE ANDROSTANE RECEPTOR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                futerPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
   164
                                 2] = LOLKGEBGSVWNYKPPADSGGKETESLLPHMADMSTYMEKGTTSFAKVTSYFKDLPTEDO
                                                                   126
                                                                                                   154 ELMDAGMKTEDTTESHEKNERLIGIVLSSGGELDESLQAPSREEAAKWSQVRKDLGSLKVS 212
                                                                                                                                      12
                                                                                                                                                                                                                                      34 EEVGGPQTORVOGEKATGVHENVMTOEGGKOFFRRAMKRNAKLROTFRKGAOETTRKTRK 92
                                                                                                                                                                                                                                                                                                                                                                                                              GNIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                   TILLCARTRHYGPMFDQFYQFRPPAYLFSH:HRPFQPLAP
                                                                                                                                    HCPACKLOKCLNVGMRKDMILSAEALALRRAROAKRRAOKASLO
                                                                                                                                                                      QCQACRERKCLESGMKKEMEMSDEAVEERRALIKRKKSERTGTQPIGVQGLTEEQRMMIR 152
                                                                                                                                                                                                       EEEYGPRNCVVCGDRATGYHEHALTCEGCKGFFRRTVSKT1GP1CPF-AGRCEVSKAQRR-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF133095; AAF22567.1;
AF133094; AAF22566.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *2000 (Ref. 40) Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO0546; THYROIDHORMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO0496;
                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation: DNA binding: Nuclear protein: er: Activator.
21 86 NUCLEAR RECEPTOR-TYPE,
21 41 C4 TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1PR001728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1PR001723;
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                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                          358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRIMORMONER
                                                                                                                                                                                                                                                                                                                                                              40922 MW;
                                                                                                                                                                                                                                                                                         40.58;
                                                                                                                                                                                                                                                                                         31.3%; Score 685.5; DR 1
40.5%; Prod. No. 5.3e-48;
                                                                                                                                                                                                                                                                         54; Mismatches 112;
VIDILITHEADINTEMVOOTIKETKOLPILERSLIMEDQ
                                                                                                                                                                                                                       C4 TYPE.
                                                                                                                                                                                                                                                                                                                                                              13691F49CAD8F1ED CRC64;
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                                                                                                                                                                                                                                                                                                         1018 1;
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ORF627: ORF628:
15-JUL-1999 (Rol. 38, Created)
15-JUL-1999 (Rol. 38, Last sequence update)
OF-2000 (Rol. 40, Last annotation update)
ORPHAN NUCLEAR RECEPTOR NR113 (CONSTITUTIVE ANDROSTANE RECEPTOR)
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROLENTry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation—the European Bioinformatics finstitute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                      EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDITINE-97442417: PubMed=9295294;
Choi H. S., Chung M., Tzameli I., Simha D., Lee Y.-K., Seol
PROSITE: PS00031: NUCLEAR_RECEPTOR;
Receptor: Transcription regulation;
Zinc finger; Activator; Alternative
                                                                                                                         Pram; PF00104; hormone_rec; 1
Pram; PF00105; zf=C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 272:23565-23571(1997).
-!- FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                      PRINTS; PROUS46; THYROIDHORMR
                                                                                        PRINTS: PRODUCTS: PRODUCTS:
                                                                                                                                                               InterPro: IPR001728;
InterPro: IPR001728;
                                                                                                                                                                                                    InterPro; IPRO01628;
                                                                                                                                                                                                                                    InterPro: IPR000324;
                                                                                                                                                                                                                                                       MGD: MG1:1346:307; Nr1i3.
                                                                                                                                                                                                                                                                                                                            or send an email to licensewish sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Differential transactivation by two isoforms of the orphan nuclear hormone receptor CAR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mas musculas (Mouse)
                                                                     PRINTS: PROUSSB; STRDHORMONER
                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
ALLERNATIVE PRODUCTS: 2 ISOFORMS; CARL (SHOWN HERE)
ARE PRODUCED BY ALTERNATIVE SPLICING. CAR2 DOES NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELEMENTS THAT CONTROL EXPRESSION OF THE RETINGIC BETA 2 AND ALCOHOL DEHYDROGENASE 3 GENES. SUBUNIT: HEFERODIMER OF NRILL3 AND KXR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRT SUHFAMILY
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                                                                                                                                                                                                                                                                                          AF009427;
                                                                                                                                                                                                                                                                         AF009328;
                                                                                                                                                                                                                     1PR000536;
                                                                                                                                                                                                                                                                      AAC53349.1;
AAC53350.1;
                                                                                         STROIDFINGER
VITAMINDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sclurognathi; Muridae;
                DNA-binding; Nuclear protein;
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               RESULT 14
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Best Local Sin
Matches 150;
SEQUENCE OF 7-401 FAVOR...... Hipakka R.A., Lido S.;
Song C., Konkontis T.M., Hipakka R.A., Lido S.;
Song C., Konkontis T.M., Hipakka R.A., Lido S.;
Song C., Konkontis T.M., Hipakka R.A., Lido S.;
"Ubiquitous receptor: a novel receptors.";
by retinoic acid and thyroid hormone receptors.";
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRANDED OLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE SPOUENCE 5'-AGGTCA-3' AND 4-NT SPACING (DR-4).
                                                                                                                                                                                                                                                                                                                                                                  p55055: Q12970;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
0XYSTEROLS RECEPTOR LXR-HETA (LLYEK X RECEPTOR BETA) (NUCLEAR ORPHAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
ZN_FING
ZN_FING
VARSPLIC
VARSPLIC
                                                                                                                                                            Shinar D.M., Endo N., Rutledge S.J., Vogel R., "NER, a new member of the gene family encoding hormone nuclear receptor.";
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                               Gene
                                                                                                                                                                                                       MEDLINE=95011628; PubMed=7926814;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                            NR1H2 OR LXRB OR UNR OR
                                                                                                                                                                                                                                                                                                                                            RECEPTOR
                                                                                                                                                                                                                                                                                                                                                        RECEPTOR LXR-BETA) (UBIQUITOUSLY-EXPRESSED NUCLEAR RECEPTOR) (NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRH2_HUMAN
                                                                                                                SEQUENCE OF 7-461 FROM N.A.
                                                                                                                                                                                                                       TISSUE=Osteosarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                             147:273-276(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAKLMGLLADIRSINNAYSYELQRLEELSAMTPLLGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLKIMAMLTEF ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRELMDAQMKTFDTTFSHFKNERLPGVH6SGCELPESLQAPSREEAAKWSQVRKDLCSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASEEEYGPKNCVVCGDRATGYHFHALTCEGCKGFFRRTVSKT1GP1CPF-AGRCEVSKAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADEFVGGPOICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKGLHLQEPEYVLMAATALFSPDRPGVTQREEIDQLQEEMALILNNHIMEQQSRLQSRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQISLLKGAAVEILHISLNTTFCLQTENFFCGPLCYKMEDAVHAGFQYEFLESILHFHKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQTSLLKGAAFELCQLRENTVFNAETGTWECGRLSYCLEDTA-GGFQQLLLEPMLKFHYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQII.LGAHTRHVGPLFDQFVQFKPPAYL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRHCPACREOKCENVGMRKDMILSAEALALRRARQAQRRAEKASLQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RROCOACRERKCIESGMKKEMIMSDEAVEERRALIKRKKSERTGTOPLGVQGLTEEORMM
                                                                                                                                                                                                                                                                                                                                            NER)
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21
57
281
287
287
358 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
41
81
286
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37.7%;
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MISSING (IN ISOFORM CAR2).
; 4F07730FF78CADBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 680; DB 1;
Pred. No. 1.5e-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR RECEPTOR-TYPE. C4-TYPE. C4-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 461
                                                                                                                                                                          encoding the human
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                                                                                                                                                                                                                                                                                  Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356
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                                                                                                                                                             ո G.A., բե
Իuman steroid
                                                                                                                                                                                                                                                                                               Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                         Schmidt A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210
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Best Local
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ZN_FING
ZN_FING
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Tr
Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t.he
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00047; STROIDFINGER. PROSITE; PS00031; NUCLEAR_RECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00104; hormone_rec;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR000536; ... InterPro: IPR001628; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U07132;
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 449
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SUBCELLULA (CAATION: NUCLEAR (POTENTIAL).
TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NR1 SUBFAMILY.
 ACIMINSTIANT
                                                                                                                                                                                                                                                                                                                                QCRLRKCKEAGMREQCVLSEEQIRKKK--IRKQQQQESQSQSQSPVGPUGSSSSASGPGA
                                                                                                                                                                                                                                                                                                                                                                                      GHELCRYCGDKASGFHYNVLSCEGCKGFFRSVVRGGARRYACKGGGTCQMDAFMRRKCO 142
                                                                                                                                                                                                                                                                                                                                                                                                                 GPQICRVCGDKATGYHENVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a cellaboration
                                                                                                                                                                                          ADMSTYMEKGIISFAKVISYERDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWEC--
                                                                                                                                                                                                                                                 LPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKE1FSLLPHM
                                                                                                                                                                                                                                                                           SPGGSEAGSQGSGEGEGVQLTAAQELM1QQLVAAQLQCNKKSFS---
                                                                                                                                                                                                                                                                                                                                                          ACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQ---PLGVQG------
                          -TPLMQELFGI 411
                                                     PGRVEALQOPYVEALLSYTRIKRPQDQLRFPRMLMKLVSLKTLSSVHSEQVFALRLQDKK
                                                                               HRVVDQLQEQFAITLKSYIECNRPQPAHRF - - LFLKIMAMLT
                                                                                                         FLKDFTYSKDDFHRAGLQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQE
                                                                                                                                   --GRUSYCLED-TAGGEQQUULEPMLKFHYMUKKLQUHEEEYYUMQAISLESPIRPGYUQ
                                                                                                                                                                TELATISVQETVDFAKQVPGFLQLGREDQIALLKASTIFIMLLETARKYNHET---ECT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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125
1231
173
191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA61783.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA58594.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zf-C4;
 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154
107
149
461
176
196
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28.3%;
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                                                                                                                                                                                                                                                                                                     -LTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                           80;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 472; DH 1;
Pred. No. 1.1e-30;
Mismatches 11
                                                                                                                                                                                                                     ----- LGAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR RECEPTOR-TYPE C4-TYPE. C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68CE3D9F9BC5C0BE CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                             114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                     ----POSRDAROGREA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 110;
                                                                                -EFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                         388
                                                                                                                                                                                                                     271
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FFFFEER Recar to the company of the 
                                                                                  Ouery Match 21.5%; Score 469.5; DE 1
Best Local Similarity 29.1%; Pred. No. 1.7e-30;
Matches 124; Conservative 76; Mismatches 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MODSE MODSE STANDARD; PRT; 445 AA.

ONZOYS; OSGUEZ;

OMAY ZOUG (Rel. 49, Created)

OF OCT 2000 (Rel. 40, Last sequence update)

OF OCT 2000 (Rel. 40, Last annotation update)

OXYSTEROLS RECEPTOR LXK-ALPHA (LIVER X RECEPTOR)
                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen Y.E., HOTIUCHI M., DZHI V.J.;
SHDMITTER (AUG 1998) TO THE EMBL/ZeriBark/DDBJ databases.

SHDMITTER (AUG 1998) TO THE EMBL/ZeriBark/DDBJ databases.

ITS ROLE AS A SILENT DNA-HINDLE PARTNER TO AN ACTIVE LIGAND-HINDLE SUBJULT IN MEDIATING RETINULD RESPONSES THROUGH TARGET GENES DEFINED BY LARES, LAKES ARE LEG-YEYE RESPONSE SLEEMENTS CHARACTERIZED BY DIRECT REPEATS OF TWO SIMILAR HEXANDICLOTIDE HALF-SITES SPACED BY OR NUCLECTIDES. LAKES AN IMPORTANT ROLE IN THE REGULATION OF CHOLESTERGL HOMEOGRAFS.

SITES SPACED BY FORK NUCLECTIDES. LAKES AN IMPORTANT ROLE IN THE REGULATION OF CHOLESTERGL HOMEOGRAFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUEEN'E FROM N.A.
STRAIN 129/SSU; TISSUE-Liver:
MEDLINE 20156473; PubMed-10675617;
Alberti S., Steffensen K.R., Gustafsson J.-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS: PRODUCT; STROIDFINGER, PROSTTE: PSOUDST; NUCLEAR_RECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: AJ132599: CAB51952.1)
EMBL: AJ132600: CAB51952.11;
EMBL: AJ132601: CAB51953.11;
EMBL: AP085745: AAD16050.11;
MGD: MGT:1352462; NCTh3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss firstitute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural characterisation of the mouse nuclear oxysterol receptor genes LXRalpha and LXRbeta."; Gene 244:93\cdot103(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plan; PE00104; hormone rec;
Plan; PE00105; zf C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to licensemish sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR LIKE ALIPHA).
                                                                                                                                                                                                                                                                                                                              SN FING
                                                                                                                                                                                                                                                                                                                                                             ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                      ONTH-VNC
                                                                                                                                                                                                                                                                                                                                                                                                                          Zinc Linder
                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR000536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                           Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRI SUBFAMILY.
EDTESVERKESVNADEEVOORQIORVOODKATOYHENVMICEGOKGEERKAMKKNAALAC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P20393; 1A6Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPR001628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription
                                                                                                                                                                                                                                         445
                                                                                                                                                                                                                                                                    565
217
713
711
711
96
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iption regulation; DNA binding; Nuclear protein;
                                                                                                                                                                                                                                  399 R
50476 MW;
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116
156
432
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                                                                                                                                                                                                                                                                                                                           C4-TYPE.
                                                                                                                                                                                                                                                              R · · P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                         NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                     CC9A8DF38D935593 CRC64;
                                                                                     Mismatches 139;
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                                                                                     Indets 87;
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4 0 5	366 OBQFAITLKSYTECHKPQPAHKELFLKIMAMLTEFATPIM 405	0у 366	_
379	NKEDFAKAGLQVEF INPIFEFSKAMNELQLNDAEFALLIAISIESADKPNVQDGLQVERL	Db 320	_
365		υγ 307	_
319	261 VSVQETVDFAKQLPGFLQLSREDQIALLKTSAIEVMLLETSKRYNPGSESITF-LKDFSY 319	Db 261	_
306	249 YMEKGIISEAKVISYEKDIPIEDOISILKGAAFELGOLFENTVENAETGTWEGGKLSY	QY 249	_
260	DKLKVTPW-PIAPD	Db 229	_
248	189 QAPSKEEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKETFSLLPHMADMST 248	OY 189	_
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Search completed: July 11, Job time: 170 sec 2001, 09:13:20

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thyroid hormone re	2 806410	410	17.5	382	45
retinoic acid rec	2 578481	452	17.5	382.5	44
retinoic acid rec	2 S13512	455	17.6	384	3
retinoic acid rec	2 S05051	448	17.6	386	42
retinoic acid rec	2 151256	444	17.6	386	41
retinoie acid red	2 A41977	459	17.7	387	40
retinoic acid rece	2 S02827	448	17.7	387	39
thyroid bormone re	1 TVXI.TA	418	17.8	389	38
thyroid hormone i	1 QRMSA1	410	17.8	389	37
thyroid hormone re	2 A32608	614	17.8	389.5	36
thyroid hormone re	2 S09178	410	17.8	390	S
retinoic acid rec	2 A43786	448	18.0	393	4
retinoic acid reco	2 A56558	464	18.0	394	ښ
thyroid hormone re	2 814416	410	18.0	394	2
thyroid hormone re	2 A40917	410	18.0	394	31
thyroid hoimone re	L TVCHVR	408	α.4	401.5	30

ALIGNMENTS

thyroid hormone receptor homolog - African clawed troq C:Species: Xenopus Laevis (African clawed troq) C:Decies: Zenopus Laevis (African clawed troq) C:Date: 20-May-1994 **sequence_revision 26-May-1995 **text_change 20-Sep-1999 C:Accession: S41497 **s84486 C:Accession: S41497 **s84486 R:Smith, D.P.; Mason, C.S.; Jones, E.A.; Old, R.W. Nucleic Acids Res. 22, 66-71, 1994 Ş B γ Ъ Ş DЬ Qγ Db ő Дb γ ₽ Qy C:Superfamily: unassigned erbA-related proteins: erbA transforming protein C:Keywords: zinc finger F:35-303/Domain: erbA transforming protein homology <ERBA> A; Molecule type: mRNA A; Residues: 1-386 <SMI> A;Title: A novel nuclear receptor supertamily member A;Reference number: \$41497; MUID:94173664 A;Accession: \$41497 A;Cross-references: EMBL:X75163; NID:g410517; PIDN:CAA53006.1; PID:g410518 A:Status: preliminary; nucleic acid sequence not shown Query Match 42.2%; Score 922.5; DH 2; Length Best Local Similarity 46.6%; Pred. No. 6.4e-65; Matches 257 133 137 376 YIECNR-POPAHRELFLKIMAMLTEF----328 FIDSGRPPSPONRLLYPKIMECLTELRTVNDIHSKOLLEIWDIGPDAIPLMREVPG 197 74 14 QQLLLEPMLKFHYMLKKLQLHEFEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKS FAKMLPYFKSLDIEDQIALLKGSVAEVSVIRFNTVFNSDINTWECGPFTYDTEDMFLAGF AKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKETFS1.LPHMADMSTYMFKG118 EEEEDASNSCGTGEDEUDGDPKICRACGDRATGYHFNAMTCEGCKGFFRRAVKKNI.KLSC EDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC 77 FAKVISYFRDLPIEDQISLLKGAAFELCOLRENTVFNAETGTWEGGRJ.SYCLEDT-AGGF PPGA-SLTPEQQHFLTQLVGAHTKTFDFNFTFSKNFR--PLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSKEEA 196 RQLFLEPLVRIHRMMRKLNLQSEEYAMMAALSIFASDRPGVCDWEKIQKLQEHIALTLKD 194; Conservative 54; Mismatches 99; Indels 69; ij Xenopus that associates with -ATPLMQELFG 410 386; 383 267 256 17] 207 homology 10;

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RESULT
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A: Residues: | 420 - SUZ -
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C:Keywords: bNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Nishikawa J.: Saito, K.: Sasaki, M.: Tomidahata, Y.: Nishihara, Biochem. Biochem. 277, 209-215, 2000 A:Tribe: Molecular cloning and functional characterization of a non-A:Reference number: JC7510: MUID:20484704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         benzoate X receptor beta. African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31 Mar 2001 #sequence_revision 41-Mar 2001 #text_change 31-Mar
A;Gene: vdr a
                d'; Gemet i es :
                                  C; Comment: This receptor is an important
                                                      A: Experimental source: intestine
                                                                         A; Cross references: DDBJ:ABU 47673
                                                                                                                                    A; Accession: JC7229
                                                                                                                                                      A; Reference number: JC7229
                                                                                                                                                                          A: Fitle: Identification of cDNAs encoding
                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 270, 40 45,
                                                                                                                                                                                                             R;Suzuki, T.; Suzuki, N.; Srivastava, A.S.; Kurokawa, T.
                                                                                                                                                                                                                                 C:Accession: JC7229
                                                                                                                                                                                                                                                                        C:Species: Paraliehthys olivaceus
                                                                                                                                                                                                                                                                                        vitamin b receptor subtype a - Paralichthys olivacens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTESHKPPSPQNKLLYPKIMECLTELRTINDTHSKQLMEIWDIQPDYTPLMKEVPG
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47.1%; Pred. No. 6.5e-65;
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C)Supertamily: unassiqued erbA related proteins; erbA transforming protein homology C;Keywords: bone; calcium transport; DNA binding; hormone receptor; intestine; vitami

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A:Molecule type: mKNA
A:Residues: 1 448 -ELA.
A:Residues: 1 448 -ELA.
A:Residues: reterences: EMBL:Ul2641: NID:q595500: PHN:AAA56725.1: PID:q595501
C:Superfamily: unassigned erbA related proteins: erbA transforming protein
C:Keywords: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Accession: 150451
k:Eluroussi, M.A.: Prahl, J.M.; Deluca, H.F.
Proc. Natl. Acad. Sci. U.S.A. 91, 11596-11600, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vitamin b receptor isoform A - Japanese quail
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 13-Sep_1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: The avian vitamin D receptors; primary structures and their origins A;Reterence number: 150451; MUID:95062315
A;Accession: [5045]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:42-362/Domain: erbA transforming protein homology - ERBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.1%;
Best Local Similarity 38.8%;
135 ALKESLKPK-LSEEQQKVINILLEAHHKTFDTTYSDFNKFRPPVKSKFSSSTATHSSSVV
                                                                       133 FGTQPLGVQGLTEEQRMMIRELMDAQMKTEDTTFSHFKNFRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 PGFRDLTAEDQIALLKSSAIELIMLRSNQSFSLEDMSWSGGGPDFKYCINDVIKAGHTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 SYFROLPTEDOISLLKGAAFELGQLRFNTVFNAETGTWEGG - RLSYGLED TAGGROOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>-</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379 CNRPQPAHRELELKIMAMLTEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *19 LLEPMLKFHYMLKKLQLHEEEFYVLMQA1SLESPDRPGVLQHRVVLQLQEQFA11LKSY1E 3/8
                                                                                                                                                 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 VGPDEFDRNAPRICGVCGDKATGFHENAMTCEGCKGFFKRSMKKKASFTCPF-NGSCTIT 69
                                                                                                                                                                                                             74 AKLECPEKKGAGEITEKTERQCQAGELEKGLESGMKKEMIMSDEAVEERHALIKEKKSEE 142
                                                                                                                                                                                                                                                                                        16 CESQELQSSDMETPAVGTPEFDRNVPRTCGVCGDRATGFHFNAMTCEGCKGFFRKSMKRK 75
                                                                                                                                                                                                                                                                                                                                                               17 CEDIE - SVPGKPSVNADE EVGGPQTCRVCGDKATGYHFNVMTCEGCKGFFRRAMKRN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \overset{\alpha}{\varpi}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 VNADE - EVGGEQTCRVCGDKATGYHENVMTCEGCKGEFRRAMKRNARLROPERKGAGETT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMMIRELMDAOMKTEDTTESHEKNERLE-- GVI.SSGCELDESI.QAPSREEAAKWSQVKK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN--HPGGRILYAKMIQKLADLRSINEEHSKQYRSISFQPEHSMQLTPLVLEVFG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLEPTAKEÖAGTKKTNITHEEEHAITWG1CTTSEDREGAOHVBAKAEÖTÖEKTEFSTFÖVALLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SV-DTKMNESNLLMMYQDGA----SSPDSSEENTKLSMLPHLADLVSYS1QKVIGFAKMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARMISSLYEAHHKTYDASYSDESKERPPVREGPVTRSASRAASLHSLSDASSDSENHSPE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KUNRRHOQAORIKROIDIGMMKEFILTDEEVQREKEMILKRKEEEAAKEAMKPX-LNEEQ LVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKTKROCQACRIRKCIESGMKKEMIMSDEAVEERKALIKRKKSEKTGTOPLGVOGLTEEQ 147
                                                                                                                                              AMETORE - SGDCKTTKDNRRHOQACRLKROVDTGMMKEFTLTTDEEVQRKREMTLKRKEEET T-6
                                                                                                                                                                                                                                                                                                                                                                                                                                          170:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·SLQLRGEDGSVWNYKPPADSGGKETFSLLPHMADMSTYMFKG11SFAKV1
                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 9.5e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 768.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                      147; Indels 53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ATPLMQELFG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Longth 44H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                       --GVI, 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (July)
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A;Residues: 'R',58-423 <BU2>
C;Superfamily: unassigned orba-related proteins; erbA transforming protein homology C;Keywords: DNA binding; transcription regulation; zinc finger F;22-337/Domain: erbA transforming protein homology <ERBA>
F;24-44/Region: zinc finger F;60-84/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Burmester, J.K.; Maeda, N.; DeLuca, H.F. proc. Natl. Acad. Sci. U.S.A. 85, 1005-1009, 1988 A;Title: Isolation and expression of rat 1,25-dihydroxyvitamin A;Reference number: A31367; MUID:88124963 A;Accession: A31367
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C;Species: Rattus norvegicus (Norway rut)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
C;Accession: A31761; A31367
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A; Residues: 1-423 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Structure and regulation of the rat 1,25-dihydroxyvitamin A;Reference number: A31761; MUID:89071726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Burmester, J.K.; Wiese, R.J.; Maeda, N.; DeLuca, H.F. Proc. Natl. Acad. Sci. U.S.A. 85, 9499-9502, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:J04147; GB:J03630; NID:g203956; PIDN:AAA41089.1; PID:g203957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A31761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                          139 HHKTYDPTYADFRDFRPPVRMDGSTGSYSPR----PTLSFSGNSSSSSSDLYTTSLDMME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299
  250
                                             267 LPIEDQISLLKGAAFELCOLRFNTVFNAETGTWECGRLSYCLEDT --- AGGFQQLLLEPM 323
                                                                                                                                                                                                                                            158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
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                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                    21 PRICGYCGDRATGEHFNAMTCEGCKGFFRRSMKRKALFTCPF-NGDCRITKDNRRHCQAC
                                                                                                                                                                                                                                          QMKTFDTTFSHFKNFRLPGVL--SSGCELPESIQAPSREEAAKWSQVRKULCSLKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLQHKVVDQLQEQFAITLKSY IECNRPQPAHRFLFLK IMAMLTEF
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                                                                                                                                                                                                                                                                                       RLKRCVDIGMMKEFILTDEEVQRKREMIMKRKEEEALKDSLRPK-LSEEQQHIIAILLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                    PQICRVCGDKATGYHFNVMTCEGCKGFFRKAMKRNAKLRCPFRKGACEITRKTRRQCQAC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQDTSLVESIQDRLSDTLQTYIRCRHPPPGSRLLYAKMIQKLADLRSLNEEHSKQYRCLS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WTCGSNDFKYKVSDVTQAGHSMDLLEPLVKFQVGLKKLNLHEEEHVLLMA1CILSPDRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLPHLADLVSYSIQKVIGFAKMIPGFRDLTAEDQIALLKSSAIEVIMLRSNQSFTMEDMS
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LTSDDQIVLLKSSAIEVIMLRSNQSFTMDDMSWDCGSQUYKYDVTDVSKAGHTLELIEPL
                                                                                                                                                                                                                                                                                                                                    RIRKCLESGMKKEMIMSDEAVEERRALIKRKKSERIGTOPLGVOGLTEEORMMIRELMDA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOPEHSMOLTPLVLEVFG
                                                                                                                                            ----SLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGFISFAKVISYFRD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.8%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 762; DB 2;
Pred. No. 2.9e-52;
0; Mismatches 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                             249
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vitamin D receptor - human
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Sep-1999
C;Accession: A28200: 155353
C;Accession: A28200: 155353
R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, R;Baker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.P.; Hughes, M.; Mangelsdorf, D.P.; Mangelsdor
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C:Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999
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Proc. Natl. Acad. Sci. U.S.A. 85, 3294–3298, 1988
A;Title: Cloning and expression of full-length cDNA encoding human vitamin b receptor
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A;Accession: PC4019
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C:Supertamily: unassigned erbA-related proteins: erbA transforming protein homology
C:Keywords: DNA binding: transcription regulation: Zine finger
F:22-44//homain: erbA transforming protein homology <FRBA>
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A:Moleculo Type: mRNA
A:Residues: 1 427 - HAK.
A:Cross:references: GB:JO325B: NID:q340202; PION:AAA61273.1; PID:q340203
                    Askesidnes: 1 427 -GOT.

C:Superfamily: unassigned erbA-related proteins: erbA transforming protein homology
C:Keywords: DNA binding: transcription regulation: Zinc Linger
                                                                                                                                                                                                                       Rigolo, H.; Chen, K.; Prahl, J.M.; Deluca, H.F.
Biochim, Biophys. Acta 1132, 103-108, 1992
                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvedicus (Norway raf)
C;Date: 02 Dec-1994 #sequence_revision 10 Nov 1995 #fext_change 31-oct-1997
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J. Biol. Chem. 266, 7588-7595, 1991
A:Title: Vitamin D receptor expression in buman lymphocytes.
                                                                                                           A: Molecule Type: mRNA
                                                                                                                                        A: Reference number: $24174; MUID: 92379083
A: Accession: $24174
                                                                                                                                                                                                   A; Title: A single receptor identical with that from intestine/T47D cells mediates the
                                                                                                                                                                                                                                                                                 C; Accession: $24174
                                                                                                                                                                                                                                                                                                                                                                         vitamin D receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A: Molecule type: micNA
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  F:22:341/Domain: etbA transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:60-84/Region: Zinc tinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:24-44/Region: Zine tinger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross:reterences: GB:M6520B; NID:g340204; PHDN:AAA61274.1;
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Best Local .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 PPPGSHILIYAKMIQKLADLRSINEEHSKQYRCLSFQPFGSMKLTPLVLEVFG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      882 POPAHRELELKIMAMILTEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 PLIKEQVGLKKINLHEEEHVILMATCTVSPDREGVQDAALTEATQDRESNTLQTYTRCRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ž
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDSSSFSNLDLSEEDSD-----DPSVTLELSQLSMLPHLADLVSYSTQKVTGFAKMTPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMLKFHYMIKKLQI.HEEEYVLMQATSI.FSPbRPGVI.QHRVVDQI.QEQFAITI.KSYTECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDLTSELQ LVLLKSSA LEV IMLRSNESFTMDDMSWTCGNQDYKYRVSDVTKAGHSLEL LE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REKROVDIOMMKEFILTDEEVQRKREMILKRKEEEALKDSERPK ISEEQQRIIAILEDA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDEPTETIOLISTIKGAAPELCOLRENTVENAETGTWECGRESY---CLEDTAGGEOQUILLE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHKTYDPTYSDFCQFKPPVKVNDGGGSHPSKPNSRHTFS--FSGDSSSSGSDHCITSSDM-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RERKCLESOMKKEMIMSDEAVEERRALIKKKKSERTOTOPLOVOOLTEEORMMIRELMDA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLKVSTOLRGEIMSVWNYKPPADSOCKETFSLLPHMADMSTYMFKG11SFAKV1SYF 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.38;
40.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 750: DB 2: Length 427 Pred: No. 2.5e-51;
protein
homology *.ERBA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      · · · ATPLMOELFG 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
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124 ARRP--

134 GTQPLGVQGLTEEQKMMTRELMDAQMKTEDTTFSHFKNFKLP---GVLSSGGELFESLQA 190

*RUTDEQSQVIAMLVEAHHKTYDDSYSDFCRFRPPVREGPVTRSASRAASLHS

178

NGSCTTTKDNRRHOQACREKRCVD1GMMREF1LTDEEVQRKKDL1QKRKDEEAQREAERE 1/2/2

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vitamin D receptor subtype b Faralichthys ofivaceus C;Species: Paralichthys offvaceus C;Sate: 05-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 18-C;Accession: JC7230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross references: DDBJ; ABO 37674
A; Experimental source: intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Suzuki, T.; Suzuki, N.; Srivastava, A.S.; Kurokawa, Biochem. Biophys. Res. Commun. 270, 40-45, 2000
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                                                            픋
                                                                                                                                                                                                                                                                                                                                                      C:Supertamily: unassigned erbA-related proteins: erbA transforming protein
                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: vdr-b
                                                                                                                                                                                                                                                                                                                                                                                                                C;Geneties:
                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Comment: This receptor is an important factor in calcium homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArResidues: 1-425 < SUZ >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A: Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JC7230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A: Reference number: JC7229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Affittle: Identification of cDNAs encoding two subtypes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JC7230
                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 HHKTYDPTYSDFCQFRPPVKVNDGGGSHPSRPNSRHTPS--FSGDSSSSCSDHCITSSDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 PPPGSHLLYAKMIQKLADLKSLNEEHSKQYRCLSFQPECSMKLEPLVLEVFG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 POPARKELELKIMAMLTEE ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 PMLKEBYMLKKLOLHBEEYVLMQATSLESPDRPGVLOHRVVDQLJEQEATTLKSYTECNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 QMKTFDTTFSHFKNFRLPGVLSSG----CELPESLQAPSREEAAKWSQVKKDLC-----
81 KGAGETTRKTRRQCQAGRIRKGLESGMKKEMIMSDEAVEEKRALIKKKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 PRICGYCGDRATGEBENAMTCEGCKGEERRSMKRKALFTCEE-NGDCKITKDNKKBCQAC 79
                                                                                                                      22 SVPGKESVNADE-EVGGPQTCRVCGDKATGYHENVMECEGCKGEFERAMKRNARLRCPER 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 POTCRVOODKATGYHENVMTCEGCKGFFRRAMKRNARLROPFRKGACETTRKTRROCQAC
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                                                            TVVSTSSLASDEFDRNMPRICGVCGDKATGFHFNAMTCEGCKGFFRRSMKRKATFTCPF- 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDLP1EDQ1SLLKGAAFELCQLRFNTVFNAETGTWECGRLSY - - - CLEDTAGGFQQLLLE
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                                                                                                                                                                               171; Conservative
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                                                                                                                                                                                                                                                                                                                              calcium transport; DNA binding;
                                                                                                                                                                                                           34.28;
                                                                                          62; Mismatches 136;
                                                                                                                                                                         73; Mismatches 143; Indels
                                                                                                                                                                                                           Score 748.5; DB 2;
Pred. No. 3.3e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ATPLMOELFG 410
                                                                                                                                                                                                                                                                                                                                 intestine:
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                                                                                                                                                                                                                                         Length 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: A new orphan member of the nuclear hormone receptor superfamily that interacts A;Reference number: A56197; MUID:94158827 A;Accession: A56197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nuclear hormone receptor MH67 - human C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 20-Sep-1999 C:Accession: A56197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
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A; Residues: 1-348 <BAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Baes, M.; Gulick, T.; Choi, H.S.; Martinoli, M.G.; Simha, Mol. Cell. Biol. 14, 1544-1552, 1994
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319 LRSINEAYGYQIQHIQGLSAMMPLLQE1
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Local Similarity 40.5%; Pred. No. 6.1e-50;
hes 157; Conservative 59; Mismatches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVVCGDQATGYHFNALTCEGCKGFFRRTVSKSIGPTCPF-AGSCEVSKTQRRHCPACRLQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALQDRLSETLQAYIQLH--HPGGRLLYAKMIQKLADLRSLNEEHSKQYRSLSERPEHSMQ 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSREEAAKWSQVRKDLCSLKVS----LQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADM
                                                                                                                                                                                                                        FELCQLRFNTVFNAETGTWECGRLSYCLEDTAG-GFQQLLLEPMLKFHYMLKKLQLHEEE 339
                                                                                                                                                                                                                                                                                                                                                               HMGTMFEQFVQFRPPAHLFIHHQ - PLPTLAP - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYQISDVTKAGHTLELLEPLVKFQVGLKKLNLQEEEHVMLMAICLLSPDRPGVQDHARIE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVD
                                                                                                                                                                                                                                                                                                                                                                                                       TFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVKKDLCSLKVSLQLRGEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMK 160
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                                          FAT-----PIMQEL 408
                                                                                                                               YVLMQAISLESPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRELELKIMAMLTE 399
                                                                                                                                                                            VELCHIVLNTTFCLQTQNFLCGPLRYTIEDGARVGFQVEFLELLFHFHGTLRKLQLQEPE
                                                                                                                                                                                                                                                                                             SVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KCLDAGMRKDMILSAEALALRRAKQAQRRAQQTPVQ-----LSKEQEELIRTLLGAHTR 123
                                                                                       YVLLAAMALFSPDRPGVTQRDELDQLQEEMALTLQSY1KGQQRRPRDRFLYAKLLGLLAE
                                                                                                                                                                                                                                                                     -- VLPLVTHFADINTFMVLQVIKFTKDLPVFRSLPIEDQISLLKGAA
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A;Gene: GDB:UNR
A;Gene: GDB:UNR
A;Cross-references: GDB:389570; OMIM:600380
A;Map position: 19q13.3-19q13.3
C;Superfamily: unassigned erbA-related proteins; erbA transforming C;Keywords: steroid hormone receptor
E;85-381/Domain: erbA transforming protein homology <ERBA>
F;87-154/Domain: DNA binding #status predicted <BIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Shinar, D.M.; Endo, N.; Rutledge, S.J.; voger, K.; Roban, V.S.; Cene 147, 273-276, 1994
A;Title: NER, a new member of the gene family encoding the human steroid hormone A;Reference number: JC4014; MUID:95011628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Homo sapiens (man)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Sep-1999
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A; Residues: 1-461 <SHI>
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A;Experimental source: osteosarcoma cells SAOS-2/B10
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Best Local Similarity
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-TPLMQELFGI 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACRERKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQ - - - PLGVUG - - - - - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHELCHVCGDKASGFHYNVLSCEGCKGFFRRSVVRGGARRYACRGGGTCOMDAFMRRKCO 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLKCPFR-KGACEITRKIRKQCQ-95
                                             PGRVEALQQPYVEALLSYTRIKRPQDQLRFPRMLMKLVSLRTLSSVHSEQVFALRLQDKK
                                                                                         HRVVDQLQEQFAITLKSYIECNRPQPAHRF--LFLKIMAMLT--
                                                                                                                                         FLKDFTYSKDDFHRAGLQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADKPNVQE
                                                                                                                                                                                                                                                                                 ADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGIWEC--
                                                                                                                                                                                                                                                                                                                                                                                                                      SPGGSEAGSQGSGEGEGVQLTAAQELM1QQLVAAQLQCNKRSFS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122;
                                                                                                                                                                 --GRLSYCLED-TAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQ
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LIEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCE 183
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Pred. No. 1.9e-29;
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision

02-Jul-1996

*text_change

mouse

retinoid X receptor interacting protein No.15 -

A; Title: Isolation of proteins that interact A; Reference number: A57664; MUID: 95280959

R; Seol, W.: Choi. H.S.: Moore, Mol. Endocrinol. 9, 72-85, 199

ore, D.D. 1995

specifically

with

the retinoid

X recepto

C;Accession: 149021

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RESULT
A55043
                                                                                                                         A:Cross retorences: GB:Ull685; NID:q555751; PIDN:AAA54633.1; PID:q555752 A:Note: authors translated the codon GAC for residue 74 as Set C:Superfamily: unassigned erbA-related proteins; erbA-transforming proteins (C:Keywords: steroid hormone receptor: Zine finger E:94-4657Domain: erbA-transforming protein homology <EKBA>
                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-445 < APF>
                                                                                                                                                                                                                                                                                                                              A; Reference number: A56043;
A; Accession: A56043
                                                                                                                                                                                                                                                                                                                                                      A;Title: A novel orphan receptor specific for a subset of thyroid hormone responsive elax; Reference number: A56043; MUID:95021230
                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Cell. Biol. 14, 7025-7035, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                R;Aplel, R.; Benbrook, D.; Lernhardt, E.; Ortiz, M.A.; Salbert, G.; Ptahl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: A55043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 01-Dec 1995 #sequence_revision 01-Dec 1995 #text_change 24-Sep-1999
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CJSpecies: Rattus norvegicus (Norway rat)
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A:Status: preliminary: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-446 - kRS+
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Query Match
Best Local Similarity
Matches 12% Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHELCRVCGDKASGFHYNVLSCEGCKGFFRRSVVHGGAGRYACRGSGTCOMDAFMRRKCO 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOOPYVEALLSYTRIKKPQDQLREPRMLMKLVSLKTLSSVHSEOVEALRLODKKLPPLLS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSKDDFHRAGLQVEFINPIFEFSRAMRRIGIDDAEYALLIAINIFSADRPNVQEPSRVEA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOLED TAGGEQQUELEPMLKEHYMLKKLQLHEEEYVLMQATSLESPDRPGVLQHRVVDQ
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     Conservative
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21.1%; Score 461.5;
28.9%; Pred. No. 1.2c
tive 75; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.2%; Score 463; 28.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 9.2e-
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1.2e-28;
chos 141;
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                                               DH 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   · · · A.H.B. · · · · · P.F.A · ·
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                                               Length 445;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 104;
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87;
                                                                                                                                                                           protein homology
Gaps
12;
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orphan nuclear receptor GR-1 - rat
C.Species: Rattus norwequeus (Norway rat)
C.Species: Rattus norwequeus
C.Accession: 159364; 159264
R.Teboul, M.: Enmark, E.; Li, Q.; Wikstrom, A.C.; Felto-Huikko, M.: Gustats
                                                                                                                                                                                                                                                  C:Superfamily: unassiqued erbA-related proteins; erbA-transforming protein homology C:Keywords: DNA binding; zine finger F:76:466/Domain: erbA-transforming protein homology <ERBA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: Sprague-Dawley, hepatic R; Sond, C.; Kokontis, J.M.; Hilpakka, K.A.; Liao, Proc. Natl. Acad. Sci. U.S.A. 91, 10809-10813, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krieboul, M.: Ehmark, E.; Li, Q.; Wikstrom, A.C.; Pelto-Huikko, Proc. Natl. Acad. Sci. U.S.A. 92, 2096-2100, 1995
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                                                                                                                                                                                                                                                                                                                                                                                              A: Molecule type: mRNA
A: Residues: 1-32,77,34-51,55-218,77,220-446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: 159264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Title: Obiquitous receptor: a receptor that modulates gene A:Reterence number: 159264: MOID:95062154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsTitle: OK-1, a member of the nuclear receptor superfamily that interacts with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 YMEKGI ISFAKVISYFROLP IEDQISLLKGAAFELGULKENTVEN - AETGIMEGGKLSY
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74 GHELCHVCGDKASGEHYNVLSCEGCKGFFRRSVVHGGAGRYACKGSGTCQMDAFMRKKCQ 133
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                                                       37 GPQ10RVGGDKATGYHENVMT0EGCKGFFRRAMKRNARLROPFR - KGA0ETTRKTRKQCQ 95
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                             Similarity
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                                                                                                               Conservative
                                                                                                                                         21.1%; Score 461; DB 2; 28.1%; Pred. No. 1.3e-28;
                                                                                                               78;
                                                                                                               Mismatches
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                                                                                                                                                                      Length 446.
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earch completed: July 11, 2001, 09:11:08 ob time: 73 sec

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Maximum DB
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seq length: 2000000000
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3: /SIDS#/gcqdata,
4: /SIDS#/gcqdata,
5: /SIDS#/gcqdata,
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2187
1 LEVRPKESWNHADFVHCEDT.....AMLTEFATPLMQELFGITGS 414
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1.	10 216	9 216	8 2167	7 216	6 216	5 216	4 216	3 216	2 216	1 218	No. Score
_	-		7 99.1								1
434	437	473	473	473	473	466	457	457	434	414	Query Match Length DB
20	20	20	20	20	20	20	20	20	20	20	1
AAY21799	AAY09515	AAY09516	AAY15933	AAY15936	AAY25411	AAY25410	AAY15932	AAY16035	AAY15931	AAY42691	ID
Human steroid and	Human vitamin D re	Human vitamin D re	A human intranucle	A human intranucle	Human nNR7-1 prote	Human nNR7 partial	A human intranucle	A human intranucle	A human intranucle	Human pregnane X r	Description

Claim 4; Fig lA-D; 69pp; English.

New human prequame X receptor, used to identify specific modulators agents that induce expression of cytochrome P-450 mono-oxygenase -

pur.

Human retinoid rec	AAW40072	19	472	۳.	424.5	<u>4</u> ت
Sequence encoded b	AAP80921	9	456		426	44
Lacilia cuprina ec	AAW71297	19	757	4	26.	43
L cuprina ecdysone	AAH67096	22	757		28.	42
EcR polypoptide su	AAY28603	20	757		28.	41
XR2. Homo sapiens	AAR33744	14	440		446.5	40
LXR-alpha, orphan	AAW03326	17	447		56.	39
Rat sbiquitous nuc	AAW25035	18	443		S	38
Rat ubiquitous nuc	AAR74739	16	443		457	37
OR-1 orphan recept	AAR94169	17	446		461	36
Retinoid X recepto	AAR99736	17	446		464	ω U
Human foetal lung	AAR96234	17	461		465	34
Mouse CNREB-1. Mu	AAY32374	21	445	21.3	466.5	ندا لدا
	AAW25034	18	460		470	32
NER receptor poten	AAR98140	17	461		472	31
Human steroid rece	AAR97982	17	461		472	30
Human recombinant	AAR52980	15	461		472	29
Human ubiquitous n	AAR74738	16	460		472	28
vitamin D	S	14	367		593	27
	52	20	356		656	26
Rat vitamin 🗀 rece	AAW37261	19	356		656	25
Mouse CAR receptor	90	20	358		680	24
กแง	AAY17872	20	357	31.5	688.5	23
Human CAR receptor	AAR41346	14	348		726	22
Human CAR receptor	AAW93902	20	348		731	21
Constitutivery act	AAW32536	18	348	33.4	731	20
vitamir D	AAY09035	20	477	ω 4. ω	750	19
vitamin D	AAY09036	20	450		750	18
Human vitamin D re	AAY09064	20	427	34.3	750	17
Human vitamin D re	AAW68156	19	427	34.3	750	16
Rat vitamin b rece	AAW47509	19	423	34.7	759	15
4	AAW94623	20	423		762	14
Xenopus orphan rec	AAR98521	17	386	41.6	910.5	13
HISO Preduding V 16	AA142003	6	010	00.	1 1 1 1	į

ALIGNMENTS

RESULT AAY42691 $\begin{array}{c} \mathsf{C} \times \mathsf{$ AAY42691 standard; Protein; 414 AA WPI; 1999-601202/51. N-PSDB; AAZ07997. Kliewer SA, Willson TM; 27-MAR-1998; 26-MAR-1999; WO9948915-Al Homo sapiens cytochrome P-450 mono-oxygenase; drug interaction; hPXR Human; nuclear_receptor; pregnane X receptor; PXR; CYP; CYP3A4; Human pregnane X receptor (hPXR). 17-JAN-2000 AAY42691; (GLAX) GLAXO GROUP LTD. 30-SEP-1999. (first entry) 9808-0079593 99WO-US06737

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RESULT
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100.0% Score 2187; DB 20; Length 414;
Hest Lacal Similarity 100.0% Pred, No. 4.20-209;
Matches 414; Conservative 0; Mismalches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides an isolated human nuclear receptor (designated pregname x receptor, PXR) that binds to a cytochrome P 450 mono-exygenase (CYP) promoter. The hPXR is used to identify: its specific modulators, and compounds that induce CYP3A4 expression (i.e. to identify drug interactions, since CYP3A4 is involved in many biotransformations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drugs). The modulators are potentially useful for: associating particular diseases and conditions with PXR and for treating such conditions. Antibodies raised against hPXR can be used for determination and
                                                                                                                                                                                                                                                              A human intranuclear receptor protein
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MP1; 1999 450440/30
                                                            11 - AIIG 1997;
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                                                                                                                                                                                    Homo sapreus
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                           (NISB.) JAPAN TOBACCO
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Best Local Similarity 95.4%;
07-AUG 1998;
                                                                                                                                                     A human intranuclear receptor protein
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                                                               A human intranuclear
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ilarity 95.4%;
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identification; downstream target gene; cell proliferation;
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                                                                                                                                                                          Query Match
Best Local S
Matches 414
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                                                                                                                                                                                                                                                               of various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A human intranuclear receptor protein
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                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 32-35; 38pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                            New intranuclear receptor protein - useful for drug development
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (NISB ) JAPAN TOBACCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; intranuclear receptor protein; drug development; diagnosis;
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                                                                                                                                                                                                                                                                        he present sequence represents a human intranuclear receptor prime nucleic acid sequence was isolated from a human adult cDNA library using a swellfish ANO23 derived probe. The protein can be used for the development of drugs and diagnosis and treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
181 GCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLL
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                                                                                                                                     1 LEVRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEG 60
                                                                                                                                                                                      Local Similarity
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                                                                                    CKGFFRRAMKRNARLRCPFRKGACEITKKTRROCQACRLRKCLESGMKKEMIMSDEAVEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                   1999-350330/30
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                                    RRALIKRKKSERTGTQPLGVQGLTEEQRMMIREIMDAQMKTFDTTFSHFKNFRLPGVLSS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTE----
                       {\tt rralikrkksertgtqplqvqglteeqrmmirelmdaqmktfdttfshfknfrlpqvlss}
                                                                         ckgifrramkrnarlrepfrkyaceitrktrrgegaerlrkelesgmkkemimsdeavee
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                                                                                                                                                                                                                                                                                                                                                                                                      AAX59974.
                                                                                                                                                                                                                                                                                                                                                                 and treatment
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                                                                                                                                                                                                                                        473 AA;
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                                                                                                                                                                        Score 2167; DB 20;
Pred. No. 4.9e-207;
0; Mismatches 0;
                                                                                                                                                                                                  Length 473;
                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                              protein
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                                                                                                             Query Match 99.1%;
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                                                                                                                                                                                             The present sequence represents a human intranuclear receptor protein. The nucleic acid sequence was isolated from a human adult cDNA library using a swellfish ANO23 derived probe. The protein can be used for the development of drugs and diagnosis and treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A human intranuclear
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                                                                                                                                                            Sequence
                                                                                                                                                                                    ot various diseases.
                                                                                                                                                                                                                                                           Claim 2; Page 17–19; 38pp; Japanese.
                                                                                                                                                                                                                                                                                     New intranuclear receptor protein - useful for drug development and diagnosis and treatment of disease
                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-1997;
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                                                                         1 LEVRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEG
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                                                levrpkeswnhadivhcedtesvpgkpsvnadeevggpqicrvcqdkatqyhinvmtceq
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                                                                                                  Conservative
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                                                                                                           Score 2167; DH 20;
Pred. No. 4.9e-207;
                                                                                                  0; Mismatches
                                                                                                                         DH 20;
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                                                                                                                       Length 474;
                                                                                                  Indels
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                                                                              polypeptide. Human VDRR polypeptides and substances which affect VDRR signal transduction, can be used for freating metabolic, proliferative or inflammatory conditions. They can be used in the manufacture of a
                                                                                                                                                                 Claim 19; Page 22-24; 35pp; English.
                                                                                                                                                                                                                                                    N PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human: vitamin b receptor related protein; VDRR; obesity; diabetes; ancarexia; theumatoid arthritis; lipoprotein detect; hyperlipidaemia; hyperlipoproteinaemia; osteoporosis; tumour;
             hyperlipoproteinaemia and esteoperesis, themmated arthritis, benign and malign tumears, hyperproliferative skin disorders or hyperthyroidism.
                                                              medicament for treating the following conditions: obesity, diabetes,
                                                                                                                                The present sequence is a human vitamin b receptor related (VDRR)
                                                                                                                                                                                                                                                                                                   Berkeustam A,
                                                                                                                                                                                                                                                                                                                                                                                                                   31 - AUG 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperproliterative skin disorder; hyperthyroidism.
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                                                anorexia. Lipoprotein detects, hyperlipidaemia, hypercholesterolaemia or
                                                                                                                                                                                                   t rest ing
                                                                                                                                                                                                                                                                                                                                  (PHAA ) PHAKMACIA & UPJOHN AR
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                                                                                                                                                                                                vitamin b receptor related (VDRK) polypoptides, useful for
ating obesity, diabetes, anorexia and rheumatoid arthritis
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vectors encoding for expression of a VDRR
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                                                                                                                                                                                                                                                                                                                                                                                  98SE-0001148.
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polypeptide
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Best Local Similarity
Matches 414; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used for treating metabolic, proliferative or inflammatory conditions, by introducing them into a mammal. The introduced nucleic acid is then capable of transforming a cell in vivo and then polypeptide is expressed. A substance affecting VDRR signal transduction, such as an agonist or antagonist can be used for the manufacture of a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.B. The specification specifically claims the VDRR nucleic acid and polypeptide sequences given in figures 1, 4, 7 and 8, but no figures
                                                                                                                                                                                      Human: vitamin D receptor related protein; VDRK; obesity; diabetes:
autorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are given in the specification.
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              31-AUG-1998;
                                                                                    W09919354-A1
                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                          Human vitamin D receptor
                                                                                                                                                                                                                                                                                                                                                  AAY09515 standard; Protein; 437 AA
                                                                                                                                                      hyperproliferative skin
                                                                                                                                                                        hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCELPESIOAPSKEEAAKWSOVRKDLCSLKVSLOLKGEDGSVWNYKPPADSGGKETFSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REALIKEKKSERTGTQPLGVQGLTEEQEMMIRELMDAQMKTFDTTFSHFKNFKLPGVLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ekqffrramkrnarlrepfrkqaceitrktrrqeqaerlrkelesqmkkemimsdeavee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIPLMOELFGITGS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vvdqlqoqtaitlksyiecorpqpahrflflkimamltelrsinaqhtqrllriqdihpf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVDQCQEQEAITLKSY1ECNRPQPAHRELELKIMAMITE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cyrlsycledtaggtgglllepmlkfhymlkklglheeeyvlmgaisltspdrpgvlghr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 AA;
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                                                                                                                                                                                                                                                                             (first entry)
              98WO-SE01548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.1%;
95.4%;
                                                                                                                                                                                                                                            related gamma protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2167; DB 20;
Pred. No. 4.9e-207;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20; Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6,6
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31-MAR-1998; 14-OCT-1997;

98SE-0001148. 97SE-0003745.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           malign tumours, hyperproliferative skin disorders or hyperthyroidism. Nucleic acid vectors encoding for expression of a VDRR polypeptide can be used for treating metabolic, proliferative or inflammatory conditions, by introducing them into a mammal. The introduced nucleic acid is then by introducing them into a mammal. The introduced nucleic acid is then capable of transforming a cell in vivo and then polypeptide is expressed. A substance affecting VDRR signal transduction, such as an agonist or antagonist can be used for the manufacture of a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolic, proliferative or inflammatory condition. N.B. The specification specifically claims the VDRR nucleic acid and polypeptide sequences given in figures 1, 4, 7 and 8, but no figures are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anorexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, benign and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or inflammatory conditions. They can be used in the manufacture of a medicament for treating the following conditions: obesity, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signal transduction, can be used for treating metabolic, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a human vitamin D receptor related (VDRR) polypeptide. Human VDRR polypeptides and substances which affect VDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 19; Page 19-20; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New vitamin D receptor related (VDRR) polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PHAA ) PHARMACIA & UPJOHN AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LEVRPKESWNHADFVHCEDTESVPGKPSVNADEEVGGPQ1CRVCGDKATGYHFNVMTCEG 60
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atplmqelfgitgs 434
                                                                        CGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVI,QHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                        \verb|ckqffrramkrnar|| rcpfrkgace|| itrktrrqcqacr|| rkc|| esqmkkem|| imsdeavee||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \verb|mevrpkeswnhadf| vhcedtesvpg| kpsvnadeevggpqicrvcgd| katgyhfnvmtceg
                                      ATPLMOELFGITGS 414
                                                                                                                                                  cgrlsycledtaggfqqlllepmlkfhymlkklqlheeeyvlmqaislfspdrpgvlqhr
                                                                                                                                                                                                                            phmadmstymfkgiisfakvisyfrdlpiedqisllkgaafelcqlrfntvfnaetgtwe
                                                                                                                                                                                                                                               PHMADMSTYMFKGI1SFAKV1SYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWE
                                                                                                                                                                                                                                                                                                      gcelpeslqapsreeaakwsqvrkdlcslkvslqlrgedgsvwnykppadsggkeifsll
                                                                                                                                                                                                                                                                                                                                         GCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQ1.RGEDGSVWNYKPPADSGGKEIFSLI.
                                                                                                                                                                                                                                                                                                                                                                              rralikrkksertgtqplqvqglteeqrmmirelmdagmktfdttfshfknfrlpgvlss
                                                                                                                                                                                                                                                                                                                                                                                                                   RRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obesity, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.0%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anorexia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2165; DB 20;
Pred. No. 6.9e-207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   180
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RESULT 11
AAY21799
steroids particularly phytoestrogens or calcium channel blockers, to reduce steroid toxicity in subjects being treated with steroids, e.a. it cases of tuberoulosis (treated with rifampin and related compounds) breast cancer (treated with tamoxifen, raloxifen etc.) or osteoporosis (treated with Vitamin K), or to slow metabolism of theraponic steroids. Also, modulating endogenous SXR is used to treat disease, particularly an agonist is used where endogenous steroid levels are excessive (e.a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              steroids, and thus affects metabolism. SXR is a broad specificity, low-affinity receptor for reducing excessive levels of steroids in the circulation. (Ant)agonists of SXR are used to regulate metabolism of
                                                                                                                                                               Cells that express SXR are used to identify compounds likely to be
                                                                                                                                                                                                Cushing syndrome; virilism and hirsutism in women; polycystic ovarian disease; Il beta-, I?- or 21-hydroxlase deficiency; 3 beta-hydroxysteroid debydrogenase deficiency, or breast, colorectal or prostatic cancer), while antagonists are used where endogenous storoid levels are too low.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes, in response to a wide variety of natural and synthetic steroid hormones and (1v) is prominently expressed in liver and intestine. SXR regulates expression of catabolic enzymes, in response to many difference to the contract of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel nuclear receptor polypoptide, designate SXR (steroid and xemobiotic receptor). SXR (i) forms a hoter-dimer with rethooid X receptor (RXR), (ii) binds to a direct or inverted repeat response element motif based on the half-site AGTTCA, (iii) activates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New steroid and xenobiotic receptor, used to identify modulators controlling metabolism of steroids and xenobiotics, e.g. reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polycystic ovarian disease; cancer; colorectal; prostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             retinoid X receptor; P450 gene; steroid hormone; steroid metabolism; phytoestrogen; calcium-channel blocker; steroid toxicity; tuberculosis; breast cancer; osteoporosis; Cushing syndrome; virilism; hirsutism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human steroid and xenobiotic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY21799 standard; Protein; 434 AA
                             antagonist. The present sequence
                                                                  expression density of SXR, also for diagnosis and therapeutically
                                                                                                involved in undesirable drug interactions. Antibodies specific for are used in immunohistochemical testing for studying distribution/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription through response elements present in steroid-inducible P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blumberg B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SALK ) SALK INST BIOLOGICAL STUDIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-1999
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represents SXR

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Sequence

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Query Match

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Best Local
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17 - JAN - 1995;
                                                                                                                                DOMA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies raised against bPXR can be used for determination and purification of bPXR. The present sequence represents a histidine-6 tayged partial PXR (His6-PXR) sequence.
                                                                                                                                                              DOMA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interactions, since CYPBA4 is involved in many biotransformations of drugs). The modulators are potentially useful for: associating particular
                          16-JAN-1996;
                                                       25 - JUL - 1996
                                                                                     MO4027300-VJ
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                                                                                                                                                                                                                                    hydroxybenzoate; mercaptobenzoate; aminobenzoate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sertgtgplgvgglteegrmmirelmdagmktfdttfshfkhfrlpgvlssgcelpesig 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \mathsf{XOR}\text{-}6 has been isolated. The recombinant \mathsf{XOR}\text{-}6 may be used to requiate gene transcription or to raise antibodies of diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding receptor polypeptide responsive to hydroxy, mercapto or amino benzoate(s) - useful to regulate gene transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-354546/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blumberg B,
                         steroid;
                                                                Vitamin D receptor; VDR; bone density; retinoic acid derivative;
                                                                                                                                                                                                                                                                     AAW94623;
                                                                                                                                                                                                                                                                                                                                         AAW94623 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus orphan receptor 6 (XOR-6) (AAR98521) is a new member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SALK ) SALK INST BIOLOGICAL STUDIES
                                                                                                                             Rat vitamin D receptor protein VDRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fidsqrppspqnrllypkimecltelrtvndihskqlleiwdigpdatplmrevfg 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YIECNR-PQPAHRFLFLKIMAMLTEF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQLLLEPMLKFHYMLKKLQLHEEEYYLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLGVQGLTEEQRMMIRELMDAQMKTEDW FSHEKNFRLPGVLSSGCFLPESLQAPSREEA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Proposition | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDTESVPGKPSVNADEEVGGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rqlfleplvrihrmmrklnvqseeyammaalsifasyrpgvcdwekiqklqehialtlkd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fakmlpyfksldiedgiallkgsvaevsvirfntvfnsdtntwecgpftydtedmflagf 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ppga-sltpeqqhfltqlvgahtktfdfnftfsknfr--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRK-KSERTGTQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAKVISYFRDLPIEDQISLLKGAAFELCQLRENTVFNAETGTWECGRLSYCLEDT-AGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----rssdpt---qepqats--seaflmlphisdlvtymikgiis
                         bone calcium regulator; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.68;
                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 910.5; DB 17; Length Pred, No. 4e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATPLMQELFG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes rat vitamin D receptor (VDR) isotorm protein VDR1. The present sequence represents rat VDR0. VDR1 differs from the canonical form of VDR (VDR0) by lacking the anino acid sequence encoded by exon 9, but instead substitutes a short sequence (GIEPGREELRUCHVCDCE in the rat protein) encoded by the 5 end of intron 8. VDR1 has a dominant negative effect on the vitamin D signalling pathway. The isotorm protein can be used for determining bone density,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene for vitamin D receptor isoform protein which blocks vitamin D signal pathway - and production of recombinant isoform protein using it, for bone density assay and for screening compounds for vitamin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and for the screening of compounds (e.g. steroids and retinoic acid derivatives) for vitamin D activity (e.g. as bone calcium regulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX16606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-1998
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370
                                                                                                                                                        310
                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 hhktydptyadfrdfrppvrmdgstgsyspr----ptlsfsgnssssssdlyttsldmme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 QMKTEDTTESHEKNERLPGVL--SSGCELPESLQAPSREEAAKWSQVRKDLCSLKV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rlkrevdignmkefiltdeevgrkremimkrkeeealkdslrpk-lseegqhiiaillda
pgshqlyakmiqkladlrslneehskqyrslsfqpensmkltplvlevtq
                                                                                                                                                                                                                                                                                                                                                                                                                                                              psqfsnldingedsd-----dpsvtldlsplsmlphladlvsysiqkvigtakmipgfrd
                                                                            PAHRELFLK IMAMLTEF-----
                                                                                                                                                                                                                                                                                                     ltsddgivllkssaievimlrsngsftmddmswdcgsgdykydvtdvskaghtleliepl
                                                                                                                                                                                                                                                                                                                                                                             LPIEDQISILKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDT---AGGFQQILLEPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SLOLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRU 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RERKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPEGVQGETEEQRMMIRELMDA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pricgvegdratgihfnamteegekgffrrsmkrkalftepf-ngderitkdnrrhegae 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164; Conservative
                                                                                                                                                ikfqvqlkklnlheeehvll maicivspdrpgvqdaklveaiqdrlsstlqtyircrhppiller and the statement of t
                                                                                                                                                                                                                         LKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPU 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-JP02052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70: Mismatches 128;
                                                                            -----ATPLMQELEG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT

AAW47509 standard; Protein; 424 AA

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Omery Match 34.7%; Score 759; DB 19;
Best Local Similarity 40.0%; Pred. No. 5.5e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A novel cDNA sequence encodes the rat vitamin D receptor isoform protein (VDR). The isoform differs from the normal receptor (VDRO), which comprises the present sequence, in having the vitamin D response element currialled by 86 residues, and having an extra 19 residues inserted at the C terminal of this element. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; vitamin D receptor; isotorm protein; VDR1; VDR0; diagnosis; dominant negative receptor; signal transmission channel; bone density disorder; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acts as a dominant negative receptor in the vitamin D signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure: Fig 1; 46pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       density determination and for screening substances for vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N PSDB; AAV03129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WP1: 1998-051917/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09747172 A1
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09ptn2 brachydanio
076246 uca pugilat
09gph1 calliphora
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O1-MAY-2000 (TrEMBLrel. 13,
O1-MAR-2001 (TrEMBLrel. 16,
ORPHAN NUCLEAR RECEPTOR.
                                                                                                                                                                                    "Identification of a human nuclear receptor defines a new signal pathway for CYP3A induction.";

Proc. Natl. Acad. Sci. U.S. A. 95:12208-12213(1998).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: TO C4-TYPE STEKOID RECEPTOR ZINC FINGER FAMILY.

EMBL. AF084644; AAC64557.1; -.

HSSP: P10826; 1HRA.
                                                                                                                                                                                                                                                                                                          Bertilsson G., Heidrich J., Svensson K., Asman M., Jendeberg L., Sydow-Backman M., Ohlsson R., Postlind H., Blomquist P.,
                                                                                                                                                                                                                                                                                                                                            TISSUE=LIVER: MEDLINE=98445350; PubMed=9770465;
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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              DNA-binding: Nuclear protein: Zinc-finger.
                                              SMART; SM00399; ZnF_C4; 1.
                                                          PRINTS: PR00398: STRDHORMONER.
PRINTS: PR00047: STRDHORMONER.
PROSITE: PS00031: NUCLEAR_RECEPTOR: 1.
                                                                                                     InterPro: 1PR001628; ...
InterPro: 1PR001723; ...
Ptam: PF00104; hormone_rec; 1.
Ptam: PF00105; zf:-44; 1.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                               Berkenstam A.;
                                                                                                                                                                      InterPro; IPR000536; -.
 473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
 53899 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                              Receptor: Transcription regulation;
 3049D23C9B903016 CRC64
                                                                                                                                                                                                                                                                                new signating
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Query Match

99.1%;

Score 2167;

DB 4;

Length 473;

95.4%;

Pred No. 1.60-178;

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RESULT
09UJ26
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                                                                                                                                                                                                                                                                                                                                                      Homo Sapiens (Human).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                         PRINTS: PRO0047; STROIDFINGER, PROSITE; PS00031; NUCLEAR_RECEPTOR; 1. SMART; SM00399; ZDE_C4; 1.
                                                                               Plam; PE00104; hormono rec; 1.
Plam; PE00105; 21:C4; 1.
                                                                                                                                                                    1 SUBCELLULAR LOTATION: NUCLEAR (BY SIMILARITY)

† SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC

EMIL, A.1009936, CAB55490.1;
                                                                                                                                                                                                                                                                        Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
Vissing H.;
                                                                                                                                                                                                                                                                                                                                             NCB1_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        090026
                                                                    PRINTS; PRO0398; STRDHORMONER
                                                                                                              InterPro: 1PRO01723:
                                                                                                                                         InterPro: IPR000536;
                                                                                                                                                          HSSP; P10826; 1HRA
                                                                                                                                                                                                                                            hormone receptor PXK/SXR and localization to chromosome
                                                                                                                                                                                                                                                         *Identification of a novel protein isoform of the human nuclear
                                                                                                                                                                                                                                                                                                     TISSUE LIVER:
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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           DNA · binding;
                                                                                                                             InterPro: IPR001528;
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-MAY-2000 (TERMHITCL. 13, Last Sequence update)
-MAR-2001 (TERMHITCL. 16, Last annotation update)
CLEAR HORMONE RECEPTOR PERI-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | LEVRPKESWHIADEVICEDTESVFCKPSVNADEEVGGPQTCRVCCDKATCYHENVMTCEG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CKGFFRRAMKRNARTROPERKGAGETTRKTRRQOQACRERKOLESGMKKEMIMSDEAVEE 120
                                                                                                                                                                                                               J. Hum. Genet. 0:0-0(0).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATPLMOELECTICS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVDQUQEQFATTLKSYTECNRPQFABRFLFLKIMAMUTELRSINAQHTQRLLRIQDTHPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
           Nuclear protoin; Receptor; Transcription regulation;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              Q90J27
Q90J27;
                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLEC), 13, Created)
01-MAY-2000 (TrEMBLEC), 13, Last sequence update)
01-MAR-2001 (TrEMBLEC), 16, Last annotation updat
NUCLEAR BORMONE RECEPTOR PERLA.
Ptan; PF00104; hormone_rev; 1.
Ptan; PF00105; zf C4; 1.
PKINIS: PR00398; STROHORMONER.
PKINIS: PR00047; STROHDFINGER.
                                                                                                                                                                           "Identification of a novel protein isoform of the human nuclear
Exempso recentor PXRZSXK and localization to chromosome 3q12.1
                                                                                                                                                                                                        Wissing H.;
                                                                                                                                                                                                                                                                        NCB1_TaxID 9606;
                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                     InterPro: IPR001723;
                                                                 InterPro: IPR000546;
InterPro: IPR001628;
                                                                                               HSSP; Plu825; IHRA
                                                                                                       -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY: TO C4-TYPE STEROID RECEMBL: AJ009936; CAB55489.L: -.
                                                                                                                                                                hormone receptor PXR/SXR and localization to chromosome -13.3.", \;
                                                                                                                                                                                                                                   TISSUE-LIVER:
                                                                                                                                                                                                                                                SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       Mammalia; Entheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                    Bukaryota: Metazoa;
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                                                                                                                                                                                                                                                                                                    Chordata; Craniata;
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94.9%;
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                                                                                                                                                                                                                   J., Hansen C.,
                                                                                                                        TYPE STEROID RECEPTOR ZINC
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                                                                                                                                                                                                                     Tommer up N.,
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                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
NUCLEAR HORMONE RECEPTOR PRK2-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
SMART; SM00399; ZnF_C4; 1.
DNA-binding; Nuclear protein; Receptor; Transcription regulation; Zinc-finger.
                                                                     -!- SUBCELLULAR LOCATION: NUCLEAR (
-!- SIMILARITY: TO C4-TYPE STEKOID
EMBL; AJ00937; CAB55493.1; -.
HSSP: P10826; 1HRA.
                                                                                                                                                                                                                                                       Heard D.J., Holloway
Vissing H.;
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UJ23
                                                                                                                                                                                                                                                                                                       TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                              hormone receptor PXR/SXR and
                                                                                                                                                                                                                                    *Identification of
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                        InterPro;
                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLL
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                                                                                                                                                                 Hum. Genet.
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IPR000536; -.
IPR001628; -.
IPR001723; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                             J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.6%;
94.7%;
                                                                                                                                                                                                                                 novel
                                                                                                                                                                                                                                                                               Hansen C.,
                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                              localization to
                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB36DEC23C4C4200 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
                                                                                                                   (BY SIMILARITY)
D RECEPTOR ZINC
                                                                                                                                                                                                                                    isoform
                                                                                                                                                                                                                                                                             Tommerup N.,
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                                                                                                                   ZINC FINGER
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                                                                                                                   FAMILY
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Best Local
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
NUCLEAR HORMONE RECEPTOR PRR2-A.
                                                                                                                                                            Heard D.J.
Vissing H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ptam: PF00104; hormone_rec; 1.
pram: pF00105; z1-C4; 1.
prints; pR00358; STRDHORMONER.
pRINTS; PR00047; STROHDFINGER.
pROSITE; pS00031; NUCLEAR_RECEPTOR;
SMART; SM00399; ZnF_C4; 1.
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-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
-1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC
EMBL; AJ009937; CAB55492.1; -.
                                                                     Eur.
                                                                                                                   hormone receptor
                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UJ24
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                                                                                                                                           "Identification of
                                                                                                                                                                                                              TISSUE-LIVER;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
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375; Conserv
                                                                   Hum. Genet. 0:0-0(0)
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                                                                                                                                                                                      Hoiloway J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA; 48149 MW;
                                                                                                                   PXK/SXR
                                                                                                                a novel protein XR/SXR and locali
                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebruta; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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1.4e-158;
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Best Local Similarity
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PLAM: PF00105: Z1-C4; 1.
PRINTS: PR0039B: STROBERMONER.
PRINTS: PR00047: STROIDFINGER.
                                             Heard D.J., Holloway J., Hansen C., Tommerup N., Vissing H.:
                                                                                                                                                                                                                                                                        0900125
              "Identification of a novel protech isotorm of the human hormone receptor PXR/SXK and localization to chromosome
                                                                                                                       NCBI TaxID 9606;
                                                                                                                                   Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                               NUCLEAR HORMONE RECEPTOR
                                                                                                                                                                                                                                                            1,471116.0
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                                                                           TISSUE LIVER;
                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                          01 MAY 2000 (TrEMBLECT, 13, Created)
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InterPro: TPR001723; ...
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MAR-2001 (TrEMBLIOL. 16, Last annotation update)
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Best Local Similarity 94.5%;
Matches 358; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QYIDUZ: PRELIMINARY; PRT; 411 AA.
QYIDUZ:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                       STRAIN BREED NEW ZEALAND WHITE KABBIT: TISSUE KIDNEY: SAVAS U., Wister M.R., Griffin K.J., Johnson E.F.; "The rabbit premane x receptor is activated by rijampicin."; Submitted (SEP 1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                  oryctolaqus enniculus (Rabbit).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleosfomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; oryctolaqus.
NCBI_TaxID 9986;
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SMART: SM00399; ZnF_C4; l.
DNA-binding: Nuclear protein; Receptor; Transcription regulation;
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Ptam; PF00105; zf-C4; 1.
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HSSP: P10826; IHRA.
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-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY EMBL. AJ009936: CAB55491.1; -.
MEDLINE: 20092326; PubMed: 10628745
                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                         Q9UJ22
Q9UJ22;
Q9UJ22;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2001 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Kilewer S.A., Moore J.T.;
The pregnane X receptor: a promiscuous xenobiotic diverged during evolution.";
Mol. Endocrinol. 14:27-39(2000).
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FIEMBL; AF182217; AAD54426.1; -.
EMBL; AF188476; AAF31165.1; -.
                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00031; NUCLEAR_RECEPTOR; SMART; SM00430; HOLI; 1.
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   SEQUENCE FROM N.A
                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc-finger
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Local Similarity
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                                                                                                                   Primates;
                                                                                                                                                  Chordata;
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78.7%;
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Pred. No. 3.8e-138;
                                                                                                           Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BBF955EC17E2E71A CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----FATPLMQELFGIT 412
                                                                                                                                                  Vertebrata; Euteleostomi;
                                                                                                                   Hominidae;
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Willson T.M.,
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Best Local Similarity
                                                                                              091839; PRELIMINARY: PRT; 386 AA.
091839;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0RPHAN NUCLEAR RECEPTOR OF STEWOLD/THYROID SUPERPAMILY.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding; Nuclear protein; Zinc-finger.
SEQUENCE 342 AA; 39696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR EMBL; AJ009937; CAB55494.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hormone receptor PXR/SXR
-13.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vissing H.: Notloway J., Hansen C., Tommerup N., Aagaard Vissing H.: Note that is not a novel protein isotorm of the human thormone receptor PXR/SXR and localization to chromosome 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDHORMONEK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE: LIVER:
SEQUENCE FROM N.A. MEDLINE=94173664; PubMed=8127656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRU0047; STROIDFINGER SMART; SM00399; ZnF_C4; 1.
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Interpro: IPR001628: -.
Interpro: IPR001723: -.
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                                         NCBI_TaxID-8355;
                                                                     Amphibia: Batrachia; Anura; Mesobatrachia;
                                                                                    Eukaryota;
                                                        Xenopodinae;
                                                                                                                                                                                                                                                          324
                                                                                                                                                                                                                                                                                     400
                                                                                                                                                                                                                                                                                                                 264
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SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLQHKVVDQLQEQEAITLKSYIECNRPQPAHRELFLK1MAMLTE
                                                                                                                                                                                                                                                          DIHPFATPLMQELFGITGS
                                                                                                                                                                                                                                                                                                                                                                                                                                            IFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELGGLRENIVFNAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVLSSGCELPESLQAPSREBAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----FATPLMQELFGITGS
                                                                                                                                                                                                                                                                                                                 VLQHRVVDOLOEQFAITLKSY1ECNRPQPAHRFLFLK1MAMLTELRSINAQHTQRLLRIQ
                                                                                                                                                                                                                                                                                                                                                                       TGTWECGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPG
                                                                                                                                                                                                                                                                                                                                                                                                    TGTWECGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                IFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCULKFNTVFNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAVEERRALIKRKKSERTGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLP 175
                                                                                                                                                                                                                                                                                                                                                                                      Hum. Genet
                                                                                    Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                        Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VSLQLRGEDGSVWNYKPPADSGGKE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 0:0-0(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.68;
84.78;
                                                                                                                                                                                                                                                                                     414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1631.5; DB 4
Pred. No. 2.6e-132;
                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor: Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7C9467C3E9000A3A CRC64
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                                                                     Pipoidea: Pipidae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
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Best Local :
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A novel nuclear receptor superfamily member in Xenopus that associates with HXK, and shares extensive sequence similarity to the mammalian vitamin D3 receptor.*

Nucleic Acids Res. 22:66 71(1994).
Nishikawa J. I., Salto K., Sasaki M., Temidahara Y., Nishihara T. "Molecular cloning and lunctional characterization of a novel mu receptor, similar to embryonic benzoate receptor HXK.": Kiochem. Biophys. Res. Commun. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                    ORPHAN NUCLEAR RECEPTOR BXR-HETA.
Xenopus Laevis (African clawed frog).
Eukaryota, Metazoar Chordata; Ctaniala; Vertebrata;
Amphibia; Battachia; Anura; Mesobattachia; Pipoidea.
                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                                          NCHI_TaxID 8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01 - MAR
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                                                                                                                                                                                                                                                                                             Xemopodinae; Xemopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRODUCT; STROIDFINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X75163;
HSSP; P10826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bNA-binding: Nuclear protein; Receptor; Transcription regulation;
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|-MAR-2001 (TrEMBLIEL 16, Last anno
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46.6%; Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 97:10769-10774(2000)
EMBE: AF276753; AAG18374.1; -.
                                                                                                                                                                 Proc. Natl. Acad. Sci.
                                                                                                                                                                                             to both mammalian prequane X receptor
                                                                                                                                                                                                                                     Pubmed 11005856;
                                                                                                                                                                                                                                                                                                                                  Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
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                                                                                                                                                                                                          "CXR, a chicken xenobiotic
                                                                                                                                                                                                                       Handschin C., Podvinec M.,
                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                       Archosauria;
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                                                                                                                         491 AA; 43945 MW;
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                                                      Conservative
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Pred. No. 2.7e-71;
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                                                                           Score 876.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 270:40-45(2000).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
-!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC EMBL; AB037674: BAA95016.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopteryqii, Neopteryqii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopteryqii; Percomorpha; Pleuronectiformes;
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PRINTS: PRO0047; STRUIDFINGER.
PROSITE: PS00031, NUCLEAR RECEPTOR;
SMART; SM00430: HOLL: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00104; hormone_rec; 1.
Ptam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of cDNAs encoding two subtypes in flounder, Paralichthys olivaceus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki T., Suzuki N., Srivastava A.S., Kurokawa
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VGPDEFDRNAPRICGVCGDKATGFHENAMTCEGCKGFFRRSMKRKASFTCPF-NGSCTIT
                                                  VNADE - EVGGPQICRVCGDKATGYHENVMTCEGCKGFFRRAMKRNARLRCPFRKGACEIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STYMFKG I I SFAKVISYFRDLP I EDQ I SLLKGAAFELCQLRFUTVFUAETGTWECGRLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --AQP---GGLTAEQQELISILIAAHKRTFDSSFSQFQHYQPAVRLCIPGPCS---QSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTQPLGVQGLTEEQRMMIRELMDAQMKTFDTTFSHFKNFR-----LPGVLSSGCELPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFTCPFTR-SCP1TKAKRRQCQACRLQKCLDVGMRKDMIMSEEALGRRRALRLQRRLAQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001628;
IPR001723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000536;
                                                                                                                                                                                                                                         420 AA;
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY:
                                                                                                                                                                                                                                         47486 MW;
                                                                                                                                35.3%;
41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- ASLSPQLDCLDEDVL---
                                                                                                       66;
                                                                                                    Score 771; DB
Pred. No. 3.2e
66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
                                                                                                                                                                                                                                                                                           Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                         038FBF00D4F38067 CRC64;
                                                                                                                             2771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420
                                                                                                                                DB 13;
3.2e-58;
                                                                                                                                                                                                                                                                                              Transcription regulation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
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f vitamin
                                                                                                                                                         Length
                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D receptor
                                                                                                       42;
                                                                                                       Gaps
                                                  87
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                                                                                                       11;
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Similarity

Conservative

73;

Mismatches 133; 2.8e-56;

Indels

SdPS

12:

22 SVPCKPSVNADE-EVCGPQ1CRVCGDKATGYHFNVMTCECCKGFFRKAMKRNAKLRCPFR 80 4 TVVSTSSLASDEFDRNMPRICGVCGDKATGEHENAMTCEGCKGFERRSMKRKATFICPF-

Db

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RESULT
Q91874
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Ouery Match
Best Local S
Matches 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O91B74:
01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15, 01-MAR-2001 (TrEMBLrel, 16, VITAMIN D RECEPTOR B.
                                                                                                                                                                                          Pfam; PF00104; hormone_rec;
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                     MEDLINE-20200092; PubMed-10733902; Suzuki T., Suzuki N., Srivastava A.S., Kurokawa T.; Suzuki T., Suzuki N., Srivastava A.S., Kurokawa T.; "Identification of cDNAs encoding two subtypes of vitamin in flounder, Paralichthys olivaceus."; Biochem. Biophys. Res. Commun. 270.40-45(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopteryqii; Percomorpha; Pleuronectiformes;
                                                                                           DNA-binding; Nuclear protein;
Zinc-tinger
                                                                                                                           PROSITE; PS00031; NUCLEAR_RECEPTOR; SMART; SM00430; HOLI; 1.
                                                                                                                                                           PRINTS; PR00398; STRDHORMONER PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                         -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR EMBL; AB037673; BAA95015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pleuronectoidei; Bothidae; Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q91B74
                                                                                                                                                                                                                                         InterPro: IPR001628; -
                                                                                                                                                                                                                                                          InterPro: IPR000536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLEPMIKFHYMIKKLQIHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAIILKSYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGFRDLTAEDQIALLKSSAIEIIMLRSNQSFSLEDMSWSCGGPDFKYCINDVIKAGHTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYFROLP I EDQ I SLLKGAAFELCQLRENTVENAETGTWECG -- RLSYCLED - TAJGFQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARMISSLVEAHHKTYDASYSDFSRFRPPVREGPVTRSASRAASLHSLSDASSDSFNHSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN--HPGGRILLYAKMIQKLADLRSINEEHSKQYRSISFQPEHSMQLTPLVLEVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLEPLYKFQYGLKKLNLHEEEHVLLMGICLLSPDRPGYQDHARVEQLQDRLPEALQAYIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SV-DTKMNESNILLMMYQDGA----SSPDSSEENTKLSMLPHLADLVSYSIQKVIGFAKMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLCSLKV---SLQLKGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMMIRELMDAQMKTFDTTFSHFKNFRLP---GVLSSGCELPESLQAPSREEAAKWSQVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDNRRHCQACRLKRCIDIGMMKEFILTDEEVQREKEMILKRKEEEAAREAMRPR-LNEEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKTRRQCQACKLRKCLESGMKKEM1MSDEAVEERRALIKRKKSERTGTUPLGVcGLTEEO
                                                                                                                                                                                                                            IPR001723;
                                                                                425 AA; 48174 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                34.2%;
39.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
               Score 748.5;
Pred. No. 2.
                                                                                                            Receptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                7B1D49CF4C2C65E9 CRC64
                                                                                                            Transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                              DB 13;
                                                                                                                                                                                                                                                                                        2 I NC
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                                                                                                                                                                                                                                                                                         FINGER
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                               Length
                                                                                                                                                                                                                                                                                                                                                       D receptor
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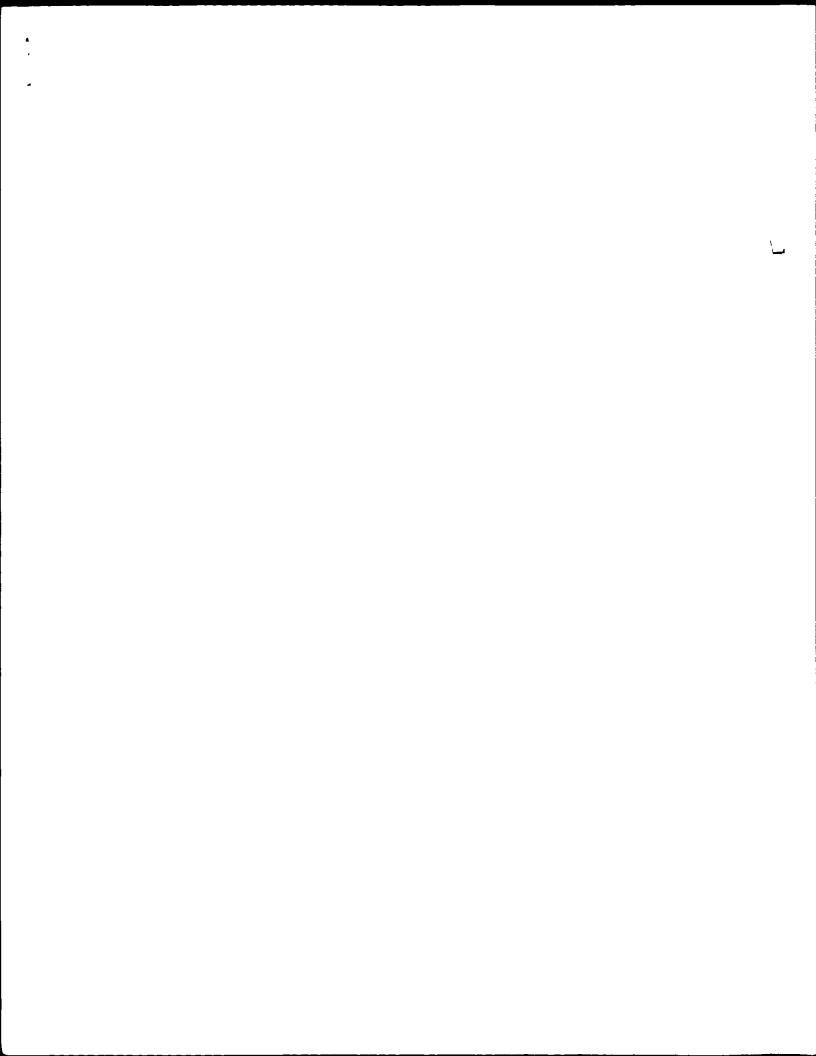
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RESULT
OPPTN2
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                                               Query Match
Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                               "Danio rerio vitamin b receptor.";
Submitted (JUL 1999) to the EMBL/GenBank/DUBL databases
I SUBCELLULAK LOCATION: NUCLEAK (BY SIMILAKITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi:
Actinopterydii: Neopterydii: Teleostei: Euleleostei: Ostariophysi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01 MAR 2001 (TYEMKI
VITAMIN D RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY 2000 (TrEMBLEEL 13, Created)
01-MAY-2000 (TrEMBLEEL 13, Last sequence update)
01-MAR-2001 (TrEMBLEEL 16, Last annotation update)
                                                                                                                                                                               PRINTS; PROD49B; STROHOMMONER.
PRINTS; PROD047; STROHOM NGER.
PROSTITE: PROD041; NUCLEAR RECEPTOR: 1.
SMART; SM00499; ZhF_C4; 1.
                                                                                                                                                                                                                                                Ptam: PF00104; hormone_rec; 1. Ptam: PF00105; zf-c4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥
                                                                                                                                                                                                                                                                                    InterPro; IPR001628;
InterPro; IPR001723;
                                                                                                                                                                                                                                                                                                                                                 I SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY EMBL; AF164512; AAF21427.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kouzmenko A.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID 7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyprinitormes: Cyprinidae: Rasborinae: Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALLAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZNJA160
                                                                                                                                                 Zine dinger
                                                                                                                                                               DNA binding: Nuclear protein; Receptor; Franscription regulation;
                                                                                                                                                                                                                                                                                                                   InterPro: IPR000536;
                                                                                                                                                                                                                                                                                                                                       HSSP; P20393; 1A6Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 / 7
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               7
               ESWNHADEVHCEDTESVPGKPSVNADEEVGGPQTCRVCCDKATGYHENVMTCEGCKGFFK-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIPLVLEVSG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALQURLSETLQAYIQLH - HPGGRLLYAKMIQKLADLRSLNEEHSKQYRSLSERPEHSMQ 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLOBOPATITIKSY LECNRPOPAHRELFIK IMAMITEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYOTSDVTKAGHTLELLEPLVKEQVGLKKLNLQEEEHVMLMATCLLSPDRPGVQDHARTE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSYSTOKVTGFAKMTPGFRELTAEDQTALLKSSATEVIMLRSNQSFNLEDMSWSGGAPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STYMEKGIISEAKVISYEKOLPIEDQISLIKGAAFELCOLKENTVENAETGEWECGK--L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSKEEAAKWSQVRKDLCSLKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPOPIANOGLIEEORMMIRELMDAOMKTFDFTESHEKNERLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYCLED-TAGGEOOLLLEPMLKEHYMLKKLQLHEEEYVLMOATSLESPDREGVLQHRVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSDASSDSFSHSPESV-DTKVNFNNLLMMYQEQGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·-·RLTDEOSQVIAMLVEAHHKTYDDSYSDFCRFRPPVREGPVTRSASRAASLIS
                                                                                                                                   454 AA;
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                   50765 MW:
                                                               34.1%; Score 746; DB-13; Length 453; 38.2%; Pred. No. Se 56;
                                               70;
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n76246;
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Chang A.C., Darica D.S., Clifton S.W., Roc B.A., Hopkins P.M.;
"Cloning of crustacean ecdysteroid receptor and retinoid-X receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota: Metazoa: Arthropoda: Crustacea: Malacostraca:
Eumalacostraca: Encarida: Decapoda: Pleocyemata: Brachyura:
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01-NOV-1998 (TIEMBLIE! 08, Last sequence update)
01-NAR-2001 (TIEMBLIE! 16, Last annotation update)
ECDYSTEROID REPERFOR HOMOLOG (FRAGMENT).
SEQUENCE
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                                                 Zimertinger.
                                                                                    PROSTIE: PS00031: NUCLEAK_RECEPTOR; SMART; SM00430: HOLI: 1.
                                                                                                                      PRINTS: PRO0398; STRDHORMONER. PRINTS: PRO0047; STROUDFINGER.
                                                                                                                                                            Ptam; PF00104; hormone_rec; 1 
Ptam: PF00105; zt-C4; 1.
                                                                                                                                                                                                               InterPro: IPR000536;
InterPro: IPR001628;
                                                                                                                                                                                                                                                     HSSP: P20393; IA6Y

    -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY
EMBL; AF034086; AAC33432.1;

                                                                                                                                                                                                                                                                                                                                         gene homologs and elevation of retinoid-X receptor mRNA by retinoic acid. ":
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                                                                   DNA binding: Nuclear protein; Receptor; Transcription regulation;
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
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Best Local Similarity 27.5%; Pred. No. 2.6e-30; Matches 117; Conservative 73; Mismatches 123; Indels 112; Gaps 39 OIGKVGGDKATGYHFNVMTCPGCKGFFRRAMKRNARHECPFFKGAGEITRKTRROGQGG 98 ::



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Result
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Gapop 10.0 , Gapext 0.5
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PCT-US95-1331-3
PCT-US95-16311-3
US-08-342-411A-4
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US-08-342-411A-4
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US-08-342-411A-4
US-08-342-411A-4
US-08-342-411A-4
US-08-373-3935-1
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Sequence 5. Appl	Patent No. 5223606	Sequence 4. Appl	Sequence 4. Appl	Sequence 2. Appl	Sequence 2. Appl:	Sequence 4. Appl	Sequence 4. Appl	Sequence 2, Appli	Sequence 2, Appl	Sequence 2. Appli	Patent No. 5223606	Sequence 1. Appli	Patent No. 5438126	Sequence 2, Appli	Sequence 2. Appl	Sequence 2, Appl	Sequence 20, App.	

ALIGNMENTS

US-08-764-870-11 Patent No. GENERAL I Sequence 11, Application US/08764870 APPLICANT: Scanlan, Thomas S APPLICANT: Baxter, John D APPLICANT: Fletterick, Robert J APPLICANT: Wagner, Richard L APPLICANT: Wester, Peter J APPLICANT: Apriletti, James W APPLICANT: West, Brian TITLE OF INVENTION: Nuclear Receptor L TITLE OF INVENTION: Binding Domains NUMBER OF SEQUENCES: 16 INFORMATION FOR SEQ ID NO: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60 FILING DATE: 13-DEC-1995 APPLICATION NUMBER: US 60 FILING DATE: 14-DEC-1995 ATTORNEY_AGENT INFORMATION: NAME: Nakamura, Jackie N REGISTRATION NUMBER: 35.9 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 6 FILING DATE: 13-DEC-1995 CORRESPONDENCE ADDRESS: SEQUENCE CHARACTERISTICS: REGISTRATION NUMBER: 35,966 REFERENCE/DOCKET NUMBER: UCAL-246/01US TELECOMMUNICATION INFORMATION: FILING DATE: 13-DEC-PRIOR APPLICATION DATA: CURRENT APPLICATION DATA: COMPUTER READABLE FORM: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CLASSIFICATION: 530 APPLICATION NUMBER: US/O FILING DATE: 13-DEC-1996 STREET: Five Pal CITY: Palo Alto STATE: CA MEDIUM TYPE: ZIP: COUNTRY: ADDRESSEE: Cooley Godward STREET: Five Palo Alto Square, TELEPHONE: LENGTH: INFORMATION: 94306 USA Patentin Release #1.0, Version #1.30 (650)843-5000 Floppy disk Nuclear Receptor Ligands and Ligand us 60/008,543 US 60/008,606 US 60/008,540 US/08/764,870 3000 El Camino Real

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Best Local Similarity 40.3%; Pred. No. 1.7e-66;
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                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5" Disketto, 1.44 Mb
COMPUTER: IBM PS/Z Model 50% of 558X
OPERATING SYSTEM: IBM P.C. DUS (Version 3.40)
SOFTWARE: WordBeartest (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DAVID D. MODIC et al. TITLE OF INVENTION: CAR RECEPTOR TITLE OF INVENTION: MOLECULES AN
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                   REFERENCE/DOCKET NUMBER: 00786/126001 TELECOMMUNICATION INFORMATION:
                                                                                                           FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massac
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                                                                                                                                                                                                            CLASSIFICATION: 435
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TELEPHONE:
                                                                 REGISTRATION NUMBER:
                                                                                            NAME:
                                                                                                                                                              APPLICATION NUMBER: 07/843,350
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/459,489
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                                                                                            Paul T. Clark
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; Patent No. 5710017
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    COMPUTER: IBM PS/2 Model 50% or 558X operating system: IBM P.C. Dos (Version 4.40) SOFTWARE: Worlderfeet (Version 5.0) CURRENT APPLICATION DATA:
                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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TIPLE OF INVENTION: CAR RECEPTORS AND RELATED
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                    APPLICATION NUMBER: 07/843,350 FILING DATE: February 26, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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STRANDEDNESS: N/A
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                                                                                                                                             APPLICATION NUMBER: US/08/458,686
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INFORMATION FOR SEQ ID NO: 10:
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REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
              COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTMARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/843,350C
                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette.
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                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 02110-2804
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TOPOLOGY: lin
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVLMQAISLESPDRPGVLQHRVVDQLQEQFAITLKSYLECNRPQPAHRELELKIMAMLTE 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEICHIVLNTTFCLQTQNFLCGPLRYTIEDGARVGFQVEFLELLFHFHGTLRKLQLQEPE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMGTMFEQFVQFRPPAHLFIHHQ-PLPTLAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCLDAGMRKDMILSAEALALRRAKQAQRRAQQTPVQ-----LSKEQEELIRTLLGAHTR 123
                                                                                                                                                                                                                    Boston
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                                                                                                                                                                                                                                                                                                                               David D. Moore et al.

VENTION: CAR RECEPTORS AND RELATED
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                                                                                                                                                                                                                                                        Fish & Richardson
February 26, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.4%; Score 731; DB 1; 40.5%; Pred. No. 9.9e-65;
                                                                                                                                                                                                                                                                                                                   MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PLMQEL 408
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                                                                                                                   , 1.44 Mb
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                                                                              3.30)
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US-07-737-736B-4
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                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/07737736B Patent No. 5260199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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TELEX: 200154
INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (627) 542-5070
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     APPLICANT: Deluca, Hector F. APPLICANT: Ross, Troy K. APPLICANT: Prahl, Jean M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM
                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                               TITLE OF INVENTION: Method Of Producing
TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 FELCQLRENTVENAETGTWECGRLSYCLEDTAG-GFQQLLLEPMLKFHYMLKKLULHEEE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 TFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCS1.KVSLQLRGEDG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 KCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPIGVQGLTEEQRMM1RELMDAQMK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                319 LRSINEAYGYQIQHIQGLSAMMPLLQEI 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 CVVCGDQATGYHFNALTCEGCKGFFRRTVSKSIGPTCPF-AGSCEVSKTQRRHCPACRLQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
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                                                                              SIREET: 411 East
CITY: Milwaukee
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                     2 I P :
                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVLMQAISLESPDREGVLOHRVVDQLQEQFAITLKSYIECNREQPAHRELELKIMAMLIE 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEICHIVLNTTFCLQTQNFLCGPLRYTIEDGARVGFQVEFLELLFHFHGTLRKLQLQEPE
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157; Conserv
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                                                                                                 411 East Wisconsin Avenue
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                                                                                                                      Carl R. Schwartz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.4%; Score 731; DB 1;
40.5%; Pred. No. 9.9e-65;
vative 59; Mismatches 100
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                                                                                                                      Quarles & Brady
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 414 277-5774
INFORMATION FOR SEQ 1D NO: 4:
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PAGES: 1005-1009
DATE: February-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Schwartz, Carl R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 TLEFSCNSSSSSSDLYTTSLOMMERSGESNLOLIGEDSD- -- DPSVTLDLSPLSMEDLEFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 GTOPLGVOGLITEEORMMIRELMDAOMKTEDTTESHEKNERLEGVL -- SSGCELEESLQAP (19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 SQDYKYDYTDYSKAGHTLELLEPLIKFQYGLKKLNLHEEEHVLLMAICIYSPDRPGYQDA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 RESYCLEDT --- ACKEROLLEDMEKEHMEKELDHIEBEEYVEMOATSLESIDREGVEGE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24. MADMSTYMEKGIISEAKVISYEKDIDIDDQISILKGAAFELGQIRENTVENAETGTWECG. 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 SREEAAKWSOVRKDLOSLKV
                                                                                                                                                          $50 NSMKLTPLVLEVEG 363
                                                                                                                                                                                                                                                                                                                                                      290 KLVEATODRESNTEQTYTRCRHPPPGSHQLYAKMTQKLADERSLNEEHSKQYRSESFQPE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 RYVIQUIQEQEATITLESYTECNEPQPAHRELELETETWAMITEE
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TITLE: 1,25-dibydroxyvitamin Di receptor coma
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ADTHORS: Maeda, No. 5250199uyo
ADTHORS: Delica, Hector F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 RURCPERKGACETERKTERROCOACKURKCLESGMKKEMIMSDEAVEERRAUTKRKKSERE 133
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                                                                                                                                                                                                                                                           · ATPLMQELEG 410
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/08330518
; Patent No. 5607967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 122; Conservative 80; Mismatches 119; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.6%; Score 472; DB 1; Longth 461; Host Local Similarity 28.3%; Pred. No. 9.20-49;
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
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329 FIKDFTYSKDDFHRAGLOVEFINPIFEFSRAMRKLGLDDAEYALLIAINIFSADRPNVQE
                                                                               272 TELATISVGETVDFAKQVPGFLQLGREDQTALLKASTTEIMLLKTARRVNHET - ECJT 428
                                                                                                                        244 ADMSTYMEKGIISEAKVISYEKDLEIDQISLLKGAAFELGOLKENTVENAETGIWEC-
                                                                                                                                                                                                     184 LPESLOAPSKEEAAKWSOVRKDLCSLKVSLOLRGEDGSVWNYKDPADSGGKETFSLLDHM 243
                                                                                                                                                                                                                                                201 SPOISEAGSQGSGEGEGEQUITAAQELMIQULVAAQLQCNKKSFS-------
                                                                                                                                                                                                                                                                                         144 ...
                                                                                                                                                                                                                                                                                                                                143 OCHERKOKEAGMREGOVESEEGIRKKK--IRKQQQQESQSQSQSPVGPQGSSSSASGPGA 100
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21MFUTER: THM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SEFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                83 CHELCKYCCOXASGEHYNVLSCECCKGEERKSYVRGGARRYACRGGGTOQMDAFMRRKCO 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 SPOTCKVCGDKATGYHENVMTGEGGKGEFKRAMKRNAKLRCPFK-KGACEITRKTRRQCQ 35
                                                                                                                                                                 ----- DOPKVTPWP---- -- ---- IGAD -- -- ROSRDAROGREA- -HE 271
                                      -GRESYCLED-TAGGFOOLLERMERFHYMERKLOLHEERYFLMOATSLESPERPGVEO 358
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| 126 East Lincoln Avenue
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Vegel, Robert
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US-08-330-283-2
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                                                                                                                                                                                                                                                          Query Match
Best Local !
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                                                                                                                                                                                                                                      Matches 122;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Friedman, Eitar
APPLICANT: Holloway, M. K.
APPLICANT: Rodan, Gideon
APPLICANT: Rutledge, Su Ja
APPLICANT: Schmidt, Azrie
APPLICANT: Yogel, Robert
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REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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201 SPGGSEAGSQGSGEGEGVQL/FAAQELMIQQLVAAQLQCNKRSFS----------
                                                                          143 QCRLRKCKEAGMREQCVLSEEQIRKKK--IRKQQQQESQSQSQSPVGPQGSSSSASGPGA 200
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                          83
                                                                                                                                                                                           37 GPQICRVCGDKATGYHENVMTCEGCKGEFRRAMKRNARLRCPER-KGACEITRKTRRQCQ 95
                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/330,283
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                                                                                                                 ACRERRCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQ---PLGVQG------ 142
                                                                                                                                                        GHELCRVCGDKASGFHYNVLSCEGCKGFFRRSVVRGGARRYACRGGGTCQMDAFMRRKCQ 142
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Schmidt, Azriel
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                                                                                                                                                                                                                                                      21.6%; Score 472; DB 1; 28.3%; Pred. No. 9.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eitan
                                       -- LTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCE 183
                                                                                                                                                                                                                                    :08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19327
                                                                                                                                                                                                                                      Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0, Version #1.25
                                                                                                                                                                                                                                                                         DB 1; Length 461;
                                                                                                                                                                                                                                      Indels 110;
                                                                                                                                                                                                                                    Gaps
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US-08-646-248-2
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; Patent No. 5939322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                            TELEFAX: (908) 594-4/2
INFORMATION FOR SEQ ID NO:
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APPLICANT:
ANTI-SENSE:
               MOLECULE TYPE: PO
                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4283
                                                                                                                                                                                                                                                                              FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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APPLICANT:
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APPLICANT:
                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,283
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 14-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                         TOPOLOGY:
                                                                       STRANDEDNESS: single
                                                                                              TYPE:
                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                              LENGTH:
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                                                                                          amino acid
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                                                                                                          461 amino acids
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126 East Lincoln Avenue
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Schmidt, Azriel
Voqel, Robert
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SEQUENCE CHARACTERISTICS:

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RESULT 9
PCT-US95 13924 2
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                        REFERENCE/DOCKET NUMBER: 19327 PCT TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                         COMPUTER REALIABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HAM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS DOS
                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS NUMBER OF SEQUENCES: 5
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                                                                                              NAME: Quagliato, Carol S. REGISTRATION NUMBER: 35,330
                 TELEFAX:
                                   TELEPHONE:
                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                         r'T'Y: Rahway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37. GPQTCRVCGDKATGYHENVMTCEGCKGFFRKAMKRNARLRCPFR-KGACETTRKTRRQCQ-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLKDFTYSKUDFHRAGLQVEFINFIFEFSRAMRRIGLUDAEYALLIAINIFSADRFNVQE
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                 (908) 594-4720
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Schmidt, Azriel
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                                         (908) 594-3809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.6%; Score 472; DB 2; Length 461; 28.4%; Pred. No. 9.26 39;
                                                                                                                                                                                                           PCT/US95/13924
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; GENERAL INFORMATION:
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PCT-US95-13931-2
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharino
APPLICANT: Rodan, Gideon
                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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HYPOTHETICAL: NO
ANTI SENSE: NO
                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANI: Schmidt, Azri
APPLICANI: Voqel, Robert
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 LPPLISEIWDV 459
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                                                                                                                                                                                                  STREET: 126 East 1
CILY: Rahway
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 ADMSTYMFKGLISFAKVISYFRDLP1FDQ1SLLKGAAFELCQLRFNTVFNAETG1WEC-- 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 SPGGSEAGSOGSGEGEGVOLTAAOELMIQOLVAAQLQCNKRSFS-----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 PÜRVEALQOPYVEALLSYTRIKRPQDQLKFPRMLMKLVSLKTI.SSVHSEOVFALRLQDKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 TELATISVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLETARKYNHET---ECIT 428
APPLICATION NUMBER:
                                          SOFTWARE:
                                                                                                                                                                 2 I P :
                                                                                                                                                                                    CHINTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 GHELCRYCGDKASGFHYNVLSCEGCKGFFRRSVVRGGARRYACRGCGTCOMDAFMRRKCO 142
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STRANDEDNESS: sir
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                                                                                                                                                                 07065-0407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application PC/TUS9513931
                                                                                                                                                                                                                                                      126 East Lincoln Avenue
                                          Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                           Schmidt, Azriel
                                                                                                                                                                                                                                                                              Merck & Co., Inc
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PCT/US95/13931
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CLASSIFICATION:

FILING DATE:

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                                                                                                                                                                                                                                             US-08-342-411A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                      sequence 2, Application US/08342411A
Patent No. 5639616
                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (908) 594-47:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Quaditato, Carol S.
REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 19316 PCT
                                                                                                APPLICANT: LIAO, Shutsung
APPLICANT: SONG, Ching
TITLE OF INVENTION: UBLOUTTOUS NUCLEAR RECEPTOR:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                    NUMBER OF SEQUENCES: 3
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                 STREET:
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STRANDEDNESS: single
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                                                   ADDRESSEE: Arnold, White & Durkee
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Houston
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                                   P.O. Box 4433
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US-08-342-411A-2
                                                                                                                                                                US-08-372-652-3
                                                                                                                 Sequence 3, Application US/08372652 Patent No. 5932699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 122; Conservative 80; Mismatches 119; Indels 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 21.5%; Score 470; DB 1; Length 460; Best Local Similarity 28.3%; Pred. No. 1.4e-38;
                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
APPLICANT: Moore, David
APPLICANT: Seol, Wonqi
APPLICANT: Choi, Huenq-Sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 18-NOV-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: FELEPHONE: (512) 418-3000 TELEFAX: (713) 789-2679 TELEX: 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: KITCHELL, BARBARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
ZIP: 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                        HRVVDQLQEQFAITLKSY1ECNRPQPAHRE--LFLK1MAMLT------EFA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                    FLKDFTYSKDDFHRAGLQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQE 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GRLSYCLED-TAGGEOOLLLEPMLKEHYMLKKLOLHEEEYVLMOALSLESPDRPGVLO 358
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Query Match
Hest Local Similarity 28.5%; Pred. No. 5.5c-48;
Matches 121; Conservative 78; Mismatches 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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440 KIWDV 444
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                                                                                                                        LOEGEATTLKSYTECNRPOPAHRE: LELKIMAMLT------EEA------FPLMQ 406
                                                                                                                                                             YSKIJDEHKAGLQVEETNETEESKAMRRIGHJDAEVALLIAINTESAJRENVQEESKVEA 379
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: GENERAL INFORMATION:
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TITLE OF INVENTION: KETINOID X RECEPTOR INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND KELATED MOLECULES AND METHOUS
NUMBER OF SECTENCES: 17
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                                                                                                                                                                                                                         190 APSKEEAAKWSOVRKDIGSLKYSLOLKGEIGSVWNYKPPADSGGKEIFSLLFHMADMSTY 249
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
320 YSKDDFHRAGLQVEFINPIFEFSRAMRRLGLDDAEYALLIAINIFSADRPNVQEFSRVEA
                                         306 YOLED TAGGEQQLLLLERMIKEHYMAKKLQLBEEFYLMQATSLESDBPGVLGVVV
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                                                                                                                               250 MEKGIISEAKVISYERDLPIEDQISLLKGAAFELCQLRENTVENAETGTWEC----GRLS
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TELEPHONE: 017/542-8906
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INFORMATION FOR SEQ ID NO: 4:
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CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                    96
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                                                                                                                                                                                                                                                                                                    37 GPQICRVCGDKATGYHENVMTCEGCKGFFRRAMKRNARLRCPFR-KGACEITRKTRRQCQ 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
ACRURKCLESGMKKEMIMSDEAVEERRALIKRKKSERTGTQPL-----
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                                                     -DQPKVTPWP-
                                                                                                                        SQGSGEGEGIQ-LTAAQELMIQQLVAVQLQCNKRSFS------
                                                                                       PSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYM
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SONG, Ching
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (713) 789-2679
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                                                   ----PQSRDARQQRFA---HFTELAIIS 260
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US-08-333-358-8
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; Patent No. 5571696
                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORE Ph.D., DAVID J.
APPLICANT: ORG MS, ESTELITA S.
APPLICANT: ORG Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIGUERE Ph.D., VINCENT MMN
APPLICANT: YAG MT. TSG-PANG MMN
TITLE OF INVENTION: NOVEL RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                        MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patchtin Release #1.0, Version #1.25
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CITY: LOS Angeles
STATE: CA
                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Reiter Ph.D., Stephen E. REGISTRATION NUMBER: 31192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/761,068
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EPTEIRPUKKKKGPAPKMLGNELCSVCGDKASGFHYNVLSCEGCKGFFKRSVIKGAHYIC 127
                    EDTESVPGKPSVNADEEVGGDQICRVCGDKATGYHFNVMICCEGCKGFFRKAMKRNARLKC 77
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                                                                                                                                                                                                                                                                                    440 amino acids
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                                                                                         Conservative
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                                                                                                                                                                                                                        protein
                                                                                                         20.9%; Score 456.5; Di
28.4%; Pred. No. 3e-37;
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                                                                                     76; Mismatches 142;
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                                                     366 QEQEATTLKSYTECNRPQPAHRPLELKIMAMLTEFAT------
                                                                                   224 "DRLRVTPWPMAP
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                                                                                                                                                                                                                         185 LPPKRSSPPQTLPQLSPEQLGMIEKLYAAQQQGARRESES - -
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                                                                                                                                                                                                                                               KTGTOPLGVOOLTEEORMMIRELMDAOMKTFUTTESHEKNEKLPGVLSSGCELPESL 188
                                                                                                                                                                              -DPHSREARQQREA---HFTELAL 255
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Search completed: July 11, 2001, 09:10:46 Job time: 51 sec

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9b_pat2:E32701
9b_pat2:E32701
9b_pat42:E32702
9b_pr4:AF061056
9b_pr4:AF084644
9b_pr4:AF084644
                                                                                                                            qb_ov:AF164512
qb_pat1:AR009748
qb_pat2:I73479
gb_pat2:E14585
gb_htg15:AC069444
gb_ro1:AF009328
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gb_ov:AF276753
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gb_rol:AF151377
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gb_om:AF182217
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gb_pr9:HSAJ9936
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Database length: -856060004
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                                                               gb_rol:AF133094
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                                                                                         qb_pat2:E32706
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                                       gb_pat2:E14584
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US-09-276-935B-14
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                                                                                      J03258 Human vitamin D recept.
AF164512 Danio rerio vitamin il
AR009748 Sequence I from patent
173479 Sequence I from patent
1818 Sequence I from patent
1819425 H.sapiens mRNA for orph
1832706 Novel nuclear receptor i
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                                       AF133094 Rattus norvegicus sti
AF133095 Rattus norvegicus str
AF009327 Mus musculus orphan u
E14584 Rat mRNA isoform for Vi
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AF011356 Gallus gallus vitamir
J04147 Rat 1,25-dihydroxyvitam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E32700 Novel nuclear receptor E32701 Novel nuclear receptor E32702 Novel nuclear receptor
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AB037674 Paralichthys olivaceu
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AF084644 Homo sapiens orphan
AF084645 Homo sapiens orphan
                         E14585 Human mRNA isoform
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AF276753 Gallus gallus xenobio
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KEYWORDS
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LOCUS E32700
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                                                                                                                                                                                                                                                                                                               Percent Similarity:
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TITLE
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gAlaMetLysArgAsnAlaArgLeuArgCysProPheArgLysGlyAlaC
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gb_pat2:AX099119
gb_pr10:HSU14534
qb_pat1:AR035536
em_pat:E11456
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US-09-276-935B-14 x E32700
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                                                                                                                luValGlyGlyProGln1leCysArqValCysGlyAspLysAlaTh;Gly
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                               TATCACTTCAATGTCATGACATGTGAAGGATGCAAGGGGCTTTTTCAGGAG
                                             TyrHisPheAspValMetThrCysGluGlyCysLysGlyPhePheArqAr
                                                                                             CTGGAGGTGAGACCCAAAGAAAGCTGGAACCATGCTGACTTTGTACACTG
                                                                                                                                                                   TGAGGACACAGAGTCTGTTCCTGGAAAGCCCAGTGTCAACGCAGATGAGG
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JAPAN TOBACCO INC
OS HOMO SADIENS (hu
PN JF 1999127872-A/
PD 18-MAY-1998 JP 1
PF 07-AUG-1998 JP 1
PR JUN YAMAMOTO,YUT
PC C12N15/09,C07K14
C01N37/53,
PC G01N37/56//(C12
C12P21/02.C12K11/19),
PC C12P21/02.C12K11/19),
PC C12N15/00,(C12N1
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FH Key
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                                                                                                                                                                                                                                                                                                                                                                                    Quality: 2167.00
Ratio: 5.234
milarity: 95.392
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Jun.Y.Y.S.S. and Naito.
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JP 1999127872-A/1.
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JP 1999127872-A/1
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/db_xref="taxon:9606"
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1 AR0355% Sequence 1 from pa
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                                                                                                                                                                                                                                                   Quality: 2167.00
Ratio: 5.234
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                                                                                                                                                                                               US-09-276-935B-14 x E32701
                                                                                                                                                      Align seq 1/1 to: E32701 from: 1 to: 1374
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OS HOMO SUPERIS
FN JP 199127872-
FD 18-MAY-1999
PF 07-AUG-199B JE
PK JUN YAMAMGTO, Y
FC C12N15/09, C07F
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Jun, Y.Y.S.S. and Naito.
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Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.
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CL2N15/09,C07K14/72,C07K16/28,Cl2N1/21,C12P21/U2,C12O1/S8, PC
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JP 1999127872-A/2
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ACTTCTACTGGAGCCCATGCTGAAATTCCACTACATGCTGAAGAAGCTGC
                                                                           TGTGGCCGGCTGTCCTACTGCTTGGAAGALACTGCAGGTGGCTTCCAGCA
                                                                                                                                                                                         ysGlnLeuArgPheAsnThrValPheAsnAlaGluThrGlyThrTrpGlu
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                                                                                                                                                                                                                                                                                                          TICAAAGGCATCAICAGCTTTGCCAAAGTCATCTCCTACTTCAGGGACTT 869
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AL Patent: UP 199127872-A 3 18-MAY-1999;
JAPAN TOBACCO INC
OS Homo sapiens (human)
PN JP 199127872-A/3
PD 18-MAY-1999
PF 07-AUG-1998 JP 1998224172
PR JUN YAMAMOTO, YUTAKA SAITO, TAKAYUKI NAITO
PC C12N15/09,C07K14/72,C07K16/28,C12N1/21,C12P21/02,C12V1/68, PC
G01N33/53,
PC G01N33/566//(C12N15/09,C12R1:91),(C12N1/21.C12R1:19). PC
C12P21/02,C12R1:19,
PC C12N15/00,(C12N15/00,C12R1:91)
CC Location/Qualifiers
FT CDS
(1) (1422).
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Jun,Y.Y.S.S. and Naito.
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/db_xref="taxon:9606"
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                                    Gaps:
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Align seq 1/1 to: E32702 trom: 1 to: 1422

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251 PheLysGLyfTeTTeSerPheAfaftysValTTeSerTytPheArqAspLe 267
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GECCATEGAGGACCAGATCTCCCTGCTGAAGGGGGCGCCGCTTTCCGAGCTGT
                                                                                         THEAMAGGEATEAGEATTHGECAMAGTEMPETERGEATTTGAGGGACTH
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ysGluLenArqPheAsuThrVaTPheAsuAlaGluThrGlyThrTtpGlu

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                                                                                                                                                                                     Submitted (21-APR-1998) Molecular Moore Drive, RTP, NC 27709, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens orphan nuclear receptor PXR mRNA, complete cds
                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                  Lehmann, J.M., McKee, D.D., Kliewer, S.A.
                                                                                                                                                                                                                                                                                                               98395173
                                                                                                                                                                                                                                                                                                                                that regulate CYPBA4 gene expression and cause drug interactions J. Clin. Invest. 102 (5), 1016–1023 (1998)
                                                                                                                                                                                                                                                                                                                                                                      The human orphan nuclear receptor PXR is activated by compounds
                                                                                                                                                                                                                                                                                                                                                                                             Kliewer, S.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                              rHisPheLysAsnPheArgLeuProGlyValLeuSerSerGlyCysGluL 184
                                                                                                                                                                                                                                           CGTGGAGGAGGGGGGCCTTGATCAAGCGGAAGAAAAGTGAACGGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTGCCTGGAGAGCGGCATGAAGAAGGAGATGATCATGTCCGACGAGGC
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                                                            TGCCAGAGTCTCTGCAGGCCCCCATCGAGGGAAGAAGCTGCCAAGTGGAGC
                                                                                                    euProGluSerLeuGlnAlaProSerArgGluGluAlaAlaLysTrpSer
                                                                                                                                         CCATTICAAGAATITCCGGCTGCCAGGGGTGCTTAGCAGTGGCTGCGAGT
                                                                                                                                                                                                                      ATCAGGGAGCTGATGGACGCTCAGATGAAAACCTTTGACACTACCTTCTC
                                                                                                                                                                                                                                                                                                      GGACTCAGCCACTGGGAGTGCAGGGGGCTGACAGAGGAGGAGCAGCGGATGATG
Quality: 2167.00
Ratio: 5.234
milarity: 95.392
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DGSVWNYKPPADSGGKE1FSLLPHMADMSTYMFKG11SFAKV1SYFRDLP1EDQ1SLL
KGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTAGGFQQ1LLEPMLKFHYMLKKLQ
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IMAMLTELRSINAQHTQRLLRIQULHPFATFLMQELFGITGS*
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SOURCE
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                                            REFERENCE
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                                                                                                                                                                                    Homo sapiens orphan nuclear receptor (PAk2) AF084644
                     Bertilsson, G.,
                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                      Homo sapiens
                                                                                                                                                                 AF084644.1 GI:3769536
                                                                                                                                                                                                                          AF084644
                                       (bases 1 to 2802)
  -Backman,M., Ohlsson,R.,
                                                                                                                                                                                                                          2802
                  Heidrich, J., Svensson, K., Asman, M.,
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                                                                                                                                                                                                                          mRNA
Postlind, H.,
                                                               Catarrhini;
                                                                               Craniata; Vertebrata; Esteleostomi,
                                                               Hominidae;
  Blomquist, P.
                                                                                                                                                                                                       mKNA.
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                       Jendeberg.i..
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REFERENCE
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Ratio: 5.234
Percent Similarity: 95.392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borkenstam, A. Identified too of a human nuclear receptor defines a new signaling pathway for CYPIA induction

Proce. Natl. Acad. Sci. U.S.A. 95 (21), 12208-12213 (1998)
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60. .1481
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L. .2802
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367 1276	ProAspArdFrottyValLouClnHtsArqValValAsptinLouClnCl FrHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	
350 1226	InfeuHischuchuchuffyrValfouMetChAlaifeSerfouPheSer 	1177
3 4 4 1 1 7 6	nLeuLeuLeud luProMet LeuLysPhellisTyrMet LeuLysLysLeuG 	
417 1126	CysclyArgLeuSerTyrCysLeuGluAspThrAlaGlyGlyPheGlnGl 	- 1
100 1076	ysGloLeuArqPheAsnThrValPheAsnAlaGluThrGlyThrTrpGlo 	
284 1026	uProlleCluAspCln1leSerleuLeutysGlyAlaAlaPheGluLeut 	- 1 00
267 976	Phetyscly11etleSerPheAlaLysVall1eSerTyrPheArqAspLe 	
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234 876	yÖlüASpÖlySerValTrpASnTyrLySProProAlaASpSerGlyGlyL 	A
217 826	GInValArqi,ysAspi.euCysSeri.euLysValSeri.euGini.euArqGl 	- 1
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184 726	rHisPheLysAsnPheArqLeuProdlyValLeuSerSerGlyGysGluL - - - - - - - - - - - - - - - - - -	- 1 -
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1 3 4 576	aValiGlodluArqArqAlaLeqlleLysArqLysLysSerGluArqThrG - - - - - - - - - - - - - - - - - - -	
526	AAGTGCCTGGAGAGGGCATGAAGAAGGAGGATGATGAGGTCGAGGCCAAGGC	477

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REFERENCE
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Sydow-Backman,M., Ohlsson,R., Postlind,H., Blomquist,P.
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JAPAN TOBACCO INC

JAPAN TOBACCO INC

OS Homo sapieus (human)

PN JP 199127872-A/9

PD 18-MAY 1998

PF 07-AUG-1998 JP 1998224172

PF 07-AUG-1998 JP 1998224172

PR 07-AUG-1998 JP 1998224172

PC C12N15/09,C07K14/72,C07K16/28,C12N1/21,C12P21/02,C12Q1/68

G01N33/53,

PC G01N33/566//(C12N15/09,C12R1:91),(C12N1/21,C12R1:19), PC

C12P1/02,C12R1:19),

PC C12P15/00,(C12N15/00,C12R1:91)

CC

FH Key Location/Qualitiers
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Jun,Y.Y.S.S. and Naito.
Novel nuclear receptor protein, its gene and utilization thereof
Patent: JP 1999127872-A 9 18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E32708.1 GI:13026815
JP 1999127872-A/9.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Quality: 2167.00
Ratio: 5.234
Percent Similarity: 95.392
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                                            | 1061 | CAGGTCCGGAAAGATCTGTGCTCTTTGAAGGTCTCTCTGCAGCTGCGGGG | 1110
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                                                                                                                                   rHisPheLysAsnPheArqLeuProGlyValLeuSerSerGlyCysGl:I. 184
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ydluAspGlySerValTrpAsnTyrLysProProAlaAspSerGlyGlyL 234
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Locus HSAJ9936
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QMKTFDTTFSHFKNFKLPGVLSSGCELPESLQAPSREEAAKWSQVKKDLASLKVSLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product "buclear hormone receptor PRFLB"
/protein_id="CAB55491.1"
/db_xret="GI:5852065"
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/protein_id="CAR55489.1"
/db_xreft="GI:§852063"
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/gence"PRR1"
/function="transcription factor"
/unte-"full length receptor"
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/product*"nuclear hormone receptor
/protein_id="CAMSS490.1"
/db_xret="G1:5852064"
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/tissue_type-"colon"
1771._3144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SILKGAAFELCOLRENTVENAETGTWECGRISYCLEDTAGGEOGLLLEPMIKFHYMIK
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AAKWSQVRKULCSLKVSLQLRGEDGSVWNYKPYADSGGKETFSLLTHMADMSTYMFKG
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SVEGKPSVNADEEVGGPQ1CKVCGDKATGYHFNVM1CEGCKGFFRRAMKKNARLECYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MTCEGCKGFFRRAMKRNAKLKCPFRKGACEITKKTKRQCQACKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="truncated receptor"
/codon_start+1
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                                                                           TTCAAAGGCATCATCAGCTTTGCCAAAGTCATCTCCTACTTCAGGGACTT 2639
                                                                                             PheLysGlyIlcIleScrPhcAlaLysYal IleScrTyrPheArgAspLe
                                                                                                                                                     AAGAGATCTTCTCCCTGCTGCCCCACATGGCTGACATGTCAACCTACATG
                                                                                                                                                                                         ysGlullePheSerLeuLeuProHisMetAlaAspMetSerThrTyrMet 250
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                                                                                                                                                                                                                                                                                                          CAGGTCCGGAAAGATCTGTGCTCTTTGAAGGTCTCTCTGCAGCTGCGGGG
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1 (bases 1 to 4337)
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Heard, D.J.
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SEAKVISYERDLETEIGTSLLKGAAFEL/QLREWIVERAAETGIWEGGRISYCLEITAG
GEQQLLLEPMLKEHYMLKKLQLREEEYVLMQATSLESPDREGVLQHRVVIQLBQEGET
TLKSY ECNREQEAHRELETIKTMAMI/TELRSTNAQHTQRILRIQDTHPEATPLMQELE
GLTGS*
2005. 3033
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| /translation "MEYR265FRRAMKRNARLKCPFRKGACEITEKTRRQCQACRLRKC
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/tunction-"transcription factor"
/note-"full length receptor"
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PATTILKSY_BCNREGEAHREI.FI.KTMAMLTEI.RSTNAQHTQRI.LRTQDTHPFATPI.MQ
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/notes="truncated receptor"
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134	ValGludliardardalakeullebysatdbysb HHHHHHHHHHHHHHHHHHHH GTGGAGGAGAGAGGGGGGCTTGATCAACGGGAAGA	17 90	
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Savas, U., Wester, M.R., Griffin, K.J. and Johnson, E.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1895)
                                                                                                                                                                                                                                                                               /gene-"NR112"
/note-"PXR"
257. .1492
                                                      /product-"pregnane x receptor"
/protein_id="AAD54426.1"
/protein_id="AAD54426.1"
/db_xref="GI:5853354"
/translation="MGGKPTISADEFEGPQTCRVCGDKANGYHENVLTCEGCKGFFRR
/translation="MGGKPTISADEFEGPQTCRVCGDKANGYHENVLTCEGCKGFFRR
TVKRNARLRCPFRKGACEITRKTRRQCQACRLRKCILESGMKKEMIMSDVAVAQRRALI
KRKKERMEAQPPGMQGLTGEQRMIJEELMDAQMKTFDTTESHERFRKDFRLPEVLGSGCE
                                                                                                                                                                                            /gene-"NR112"
/note-"PXR; nuclear receptor subfamily 1 group 1 member
zinc-finger protein; transcription factor"
/codon_start=1
HLADMSTYMFKGTINFAKVISYFRULPTEDQTSLLKGATLELCLLRFNTVFNAETGTW
ECGRLSYCVEDPEGGFQQLLVDPLLKFHYMLKKLQLHKEEYVLMQATSLFSPDRPGVV
                                           IPESLQALTEEEAGRWRQ1QEELGTMKLSLQLRGEDGSVWNYTPPADRSGKKLFSLLP
                                                                                                                                                                                                                                                                                                                                                                 /tissue_type-"kidney"
                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                                                                                                                                                 /strain-"breed New Zealand white rabbit"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryctolagus cuniculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .1895
                                                                                                                                                                                                                                                                                                                                                      1. .1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Lagomorpha; Leporidae; Oryctolagus
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234 ysGluIlePheSerLeuLeuProHisMetAlaAspMetSerThrTyrMet
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alignment_block: us-09-276-935B-14 \times AF182217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 lyThrGlnProLeuGlyValGlnGlyLeuThrGluGluGlnArgMetMet 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 GACCGTGAAACGCAACGCCCGGCTGAGATGCCCCTTCCGGAAGGGCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TGATGAAGCAGACTCCATGGGTGGAAAGCCCACCATCAGTGCAGATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 CTGGAGGTGCTATGTGAAGGCAGTGGGAAACAAGCTGGCCTTGCGCGCGTG
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                                                                                                                                                                                                                                                                                             euProGluSerLeuGlnAlaProSerArqGluGluAlaAlaLysTrpSer
GAAGACGGCAGCTCTGGAACTATACGCCCCCAGCTGACAGAAGTGGGA
                                                                                                               CAGATECAAGAAGAGCTGGGCACCATGAAGCTCTCTCTGCAGCTGCGGGGG
                                                                                                                                                                       GlnValArqLysAspLeuCysSerLeuLysValSerLeuGlnLeuArqGl 217
                                                                                                                                                                                                                                                                                                                                                                                    rHisPheLysAsnPheArgLeuProGlyValLeuSerSerGlyCysGluL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ile {\tt ArgGluLeuMetAspAlaGlnMetLysThrPheAspThrThrPheSe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGCTCAGCCGCCGGGAATGCAAGGGCTGACGGGAGAGCAGCGGATGATA 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aValGluGluArqArqAlaLeuIleLysArqLysLysSerGluArqThrG
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                                                                                                                                                                                                                                                                                                                                                        CCATTICAAGAATITICGGCTGCCGGAGGTGCTTGGCAGTGGCTGTGAGA
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                                                    yGluAspGlySerValTrpAsnTyrLysProProAlaAspSerGlyGlyL 234
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DTHPFATPLMRELFSTTDD*
a 556 c 535 g 370 t
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KENERENS'E
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371.11.1
                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTCCTGAGATTCAACACCCTGTTCAACGCAGAGACTGGCACTTGGGAG
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               Jones,S.A., Moore,L.B., Shenk,J.L., Wisely,C.B., Hamilton,G.A., McKee,D.D., Tomkinson,N.C., LeChyse,E.L., Lambert,M.H., Willson,T.M., Kliewer,S.A. and Moore,J.T.
                                                                                                                                                                                      McKee, D.D., Tomkinson, N.C., LeClayse, E.L., Lambert, M.H., Willson, T.M., Kilower, S.A. and Moore, J.T.
The pregnanc X receptor: a promiseuous xemobiotic recept diverged during evolution
                                                                                                                                                                                                                                                                                                                                                                                          Orycholagus cuniculus
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                                                                                           2 (bases 1 to 1601)
                                                                                                                       10628745
                                                                                                                                                                     Mol. Endocrinol. 14 (1),
                                                                                                                                                                                                                                                                                         Jones, S.A., Moore, L.B., Shenk, J.L., Wisely, G.B., Hamilton, G.A.
                                                                                                                                                                                                                                                                                                                                       Mammalia; Entheria; Lagomorpha; Leporidae; Oryctolagus.
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AGATGAAAACCTTTGACACCACCTTCTCCCATTTCAAGAATTTTCGGCTG
                                                  InMet Lys threheAspThrThrPheSerHisPheLysAsnPheArqLeu
                                                                                                          AGGGTGACGGGAGGAGCGGATGATAATCGAGGAGCTGATGGAGGCTC
                                                                                                                                                          ndlyLeuThrGluGluGluArgMetMetFleArgGluLeuMctAspAlaG
                                                                                                                                                                                                                     ATCIAAGAGAAGAAGAAGAAGAAGGATGGAGGCTCIAGCCGCCGGGAATGCA
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ECGKLSYCVEDPEGGFYOULVEFERDLE HEDYTSLIKGATLELCLLKENTVENAETGTW
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KRKKRERMEAQPPGMQGLTGEQRMTTEELMDAQMKTFDTTFSHFKNFKLFEVLGSGCE
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/proteiu_id="AAF31165.1"
/db_xret="G1:6901680"
/translation="MGGKPTISADEEEGPGTCKVCGDKANGYHENVLTCBGCKGFFRR
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ProGlyValLeuSerSerGlyCysGluLeuProGluSerLeuGlnAlaPr

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DEFINITION ACCESSION
                                                                                                              seq_documentation_block:
LOCUS AF031814
                  SOURCE
                                  KEYWORDS
                                                         VERSION
                                                                                                                                                                         seq_name: qb_ro1:AF031814
ORGANISM
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[[[]]]
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                                                                                                                                                              342 GGCCATGAAACGCAATGTCCGGCTGAGGTGCCCCTTCCGCAAGGGAACCT
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ysGluIleThrArgLysThrArgArgGlnCysGlnAlaCysArgLeuArg
                                                                                                                                                                                                                                                                 gAlaMetLysArqAsnAlaArgLeuArqCysProPheArqLysGlyAiaC
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Muricae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zetterstrom, R.H., Perlmann, T. and Lehmann, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kliewer,S.A., Moore,J.T., Wade,L., Standinger,J.L.,
Jones,S.A., McKee,D.D., Oliver,B.B., Willson,T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An orphan nuclear receptor activated by prequancs
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TFEMG LEFNTMEDTETOTWEGGSLAYGEEDPNGGFQKLLLDPLMKFH-MI.KKLOHK
EEYVIJMQAISLESPDRPGVVQRSVDQLQERFALTLKAYIEGSPYFAHFFLFIKIMA
VLTELRSINAQOTQQLLKIQDSHPVATPLMQELFSSTDG*

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/protoin_id "AAC39964.1"
/protoin_id "AAC39964.1"
/db xref = 101:2853.329
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/note="pregnane-activated nuclear
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1292 CTGCTCACAGGTTCCTGTTCCTGAGGATCATGGCGTCCTCACTGAGGTG 1341
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                                                                                                                                                                                   467 uGhnPh-AlaHeffhrLeaflysSerTyri1eGhrfysAsaAraProGlnP 484 h:::HHHH::::HHHH));:::HHHHHHHH:::HHHHH
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                                                                                                                                                                                                                                                                                                                                                               51 ProAspArgProGlyValLeuGlnHisArgValValAspGlnLeuGlnG1 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 yschilouArgPheAsnThrVaTPheAsuAlaGluThrGlyThrTrpGlu=300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 rHisPheLysAsnPheArgLeuProGlyValLeuSerSetGlyCysGluL 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                           {\bf AGCTGCATAAGGAGGAGTATGTGCTGCTGATGCAGGCCATCTTCCTCCT}
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Locus AF151377
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X.laovis mRNA for orphan
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                                       The nucleic acid sequence was isolated from a human adult ciNA library using a swellfish ANO3 derived probe. The protein can be used for the development of drugs and diagnosis and treatment of various diseases.
                                                                                                                                                             Claim 4; Page 22-23; 38pp; Japanese.
                                                                                                                                                                                                                        New intranuclear receptor protein - useful for drug development and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human: intranuclear receptor protein; drug development; diagnosis;
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                                                                                                                                                                                                                                                                                                                             (NISB ) JAPAN TOBACCO INC
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                                                                                                                                                                                                                      Sequence 1374 BP;
                                                                                                                                                                                                                                                                                                                                                                       of various diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                             The nucleic acid sequence was isolated from a human adult cDNA
Library using a swellfish ANO23 derived probe. The protein can
be used for the development of drugs and diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 23-25; ⊀8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New intranuclear receptor protein
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                                                                                                                  WPI; 1999-350330/30
                                                                                                                                                                 11-AUG-1997;
                                                                                                                                                                                       07-AUG-1998;
                                                                                                                                                                                                                                    JP11127872-A
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                  treatment;
                                                                                                                                                                                                                                                                                            Human; intranuclear
                                                                                                                                                                                                                                                                                                                                           04-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                          AAX59968 standard; DNA; 1422 BP
                                                                                                                                       (NISB ) JAPAN
                                                                                                                                                                                                             18-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          er 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGACCCCCAGGTGTGCTGCAGCACCGCGTGGTGGACCAGCTGCAGGA
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                                                                                                       AAY15933.
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                                                                                                                                        TOBACCO
                                                                                                                                                                 97JP-0230335
                                                                                                                                                                                      98JP-0224172
                                                                                                                                                                                                                                                                                            receptor protein; drug development; diagnosis;
                                                                                drug
                                                                                development
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The present sequence encodes a human intranuclear receptor protein The nucleic acid sequence was isolated from a human adult CDNA library using a swellfish ANO23 derived probe. The protein can

Claim 4; Page 25-27; 38pp; Japanese.

diagnosis

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allqument_block:
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Percent Similarity: 95.392
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2 3 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 HeArqGluLeuMetAspAlaGluMetLysThrPheAspThrThrPheSe 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 LysCysLeuGluSerGlyMetLysLysGluMetlleMetSerAspGluAl 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ≈
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                                                                                                                                                                                                                                                               GBACTCAGCCACTGGGAGTGCAGGGGCTGACAGAGGAGCAGCGGATGATG
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ysGlullePheSerLeuLeuProHisMetAlaAspMetSerituTyrMet
                                                                                GGAGGATĞGCAGTCTCTGGAACTACAAACCCCCAGGCCTACACTGGCGGGA
                                                                                                                               TOTTAGAGTER FOR AGGEOGRAPH CONGRESS AND AGEOGRAPHICA AGEOGRAPH TOTTAGAGE TOT
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seq_documentation_block:
1D AAZ07997 standard;
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                                                                      /SIDS8/qcqdata/geneseq/qeneseqn/NA1999.DAT:AAZU7997
                                                                                                                                                                                                                                               .PheAlaThrProLeuMetGluGluLeuPheGlyLleThrGlyS 414
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seq_name:

standard; DNA;

17 - JAN - 2000 (first entry)

Human prequane X receptor (hPXR) encoding DNA

cytochrome P-450 Human; nuclear receptor; pregname X receptor; PXR; mono-oxygenase; drug interaction; CYP: CYP3A4:

W09948915-∧1

40 · SEP · 1999

26-MAR-1999; 99WH-US06737

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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides an isolated human nuclear receptor (designated pregnane X receptor, PXR) that binds to a cytochrome P-450 mono-oxygenase (CYP) promoter. The hPXR is used to identify: its specific modulators, and compounds that induce CYP3A4 expression (i.e. to identify drug interactions, since CYP3A4 is involved in many biotransformations of drugs). The modulators are potentially useful for: associating particular diseases and conditions with PXR and for treating such conditions. Antibodies raised against hPXR can be used for determination and purification of hPXR. The present sequence represents a DNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                604
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                                                                                                                                              LysCysLeuGluSerGlyMetLysLysGluMetIleMetSerAspGluAl 117
                                                                                                                                                                                                              ysGluileThrArqLysThrArqArqGlnCysGlnAlaCysArqLeuArq 100
                                                                                                                                                                                                                                                                                                                                             TyrHisPheAsnValMetThrCysGluGlyCysLysGlyPhePheArgAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sGluAspThrGluSerValProGlyLysProSerValAsnAlaAspGluG
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                1yThrGlnProLeuGlyValGlnGlyLeuThrGluGluGlnArgMetMet 150
                                                              GGCCATGAAACGCAACGCCCGGCTGAGGTGCCCCTTCCGGAAGGGCGCCT
                                                                                                                                                                                                                                                                            TATCACTTCAATGTCATGACATGTGAAGGATGCAAGGGCTTTTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGGACACAGAGTCTGTTCCTGGAAAGCCCCAGTGTCAACGCAGATGAGG
GGACTCAGCCACTGGGAGTGCAGGGGGTGACAGAGGAGCAGCGGATGATG
                                                                                             aValGluGluArgArgAlaLeuIleLysArgLysLysSerGluArgThrG
                                                                                                                              AAGTGCCTGGAGAGGCGCATGAAGAAGGAGATGATCATGTCCGACGAGGC
                                                                                                                                                                                             GCGAGATCACCCGGAAGACCCGGCGACAGTGCCAGGCCTGCGCCTGCGC
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5.234
95.392
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	- CT 1505	1604
1603	CACCCCTTTGCTACGCCCCTCATGCAGGAGTTGTTCGGCATCACAGGT - ^ ^ ^	<u>ت</u> ر
414	PheAlaThrProLeuMetGinGluLeuPheGlyIleThrGlyS	400
1554	GCAGCATGAATGCTGAGCACAGCAGCGGGTGGTGCGGGATGCAGGAGA	1504
399		399
399	roAlaHisArqPheLeuDheLeuLysIleMetalaMetLeuThrGlu	384
1503		1454
384	UGlnPheAlaIleThrLeuLysSerTyrIleGluCysAsnArqPtoGlnP	367
1453		1404
367	ProAspArdProGlyValLeuGlnHisArqValValAspGlnLeuGlnGl	351
1403	- - - - - - - - - - - - - - - - - - -	1354
350	InLeuHisGluGluGluTyrValLeuMetGlnAlaIleSerLeuPheSer	334
1353		1304
334	nLeuLeuLeuCluProMetLeuLysPheHisTyrMetLeuLysLysLeuG	317
1303		1254
317	CysGlyArqLeuSerTyrCysLeuGluAspThrAlaGlyGlyPheGlnGl	301
1253		1204
300	ysGlnLeuArgPheAsnThrValPheAsnAlaGluThrGlyThrTrpGlu	28 4
1203		1154
284	uProlleGluAspGlnTleSerLeuLeuLysGlyAlaAlaPheGluLeuC	267
1153		1104
267 1103	PheLysGly1le1leSerPheAlaLysVallleSerTyrPheArqAspLc	251 1054
250	ysGluIlePheSorLeuLeuProHisMotAlaAspMetSerThrTyrMet	23 4
1053		100 4
234	rpAsnTyrLysProPro	217
1003		954
217	sSerLeuLysVa	201
953		904
200	euProGluSerLeuGlnAlaProSerArgGluGluAlaAlaLysTrpSer	184
903		854
184	rHisPheLysAsnPheArqLeuProGlyValLeuSerSerdlyCysGluL	167
853	HIIHHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	804
167	IleAryGluLeuMetAspAlaGluMetLysThrPheAspThrThrPheSe	151
803		754

.604 GC

seq_name: /SIDSB/qcqdata/geneseq/qeneseqn/NA1999.DAT:AAX56243

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alignment_block
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                                                                                            <u>=</u>
                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                               malian immours, hyperprolliterative skin disorders or hyperthyroidism. Nucleic acid vectors encoding for expression of a VDRK polypeptide can be used for treating metabolic, prolliterative or inflammatory conditions, by introducing them into a mammal. The introduced nucleic acid is then capable of transforming a cell in vio and then polypeptide is expressed. A substance affecting VDRK signal transduction, such as an agonist or antagonist can be used for the manufacture of a medicament for treating metabolic, prolliterative or inflammatory condition.

N.H. The specification specifically claims the VDRK mucleic acid and polypeptide sequences given in figures 1, 4, 7 and 8, but no figures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anorexia. Lipoprotein detects, hyperlipidaemia, hypercholesterolaemia or hyperlipoproteinaemia and osteoporosis, theumatoid arthritis, benign and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of inflammatory conditions. They can be used in the manufacture of a medicament for treating the following conditions: obesity, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            signal transduction, can be used for treating metabolic, proliferative or inflammatory conditions. They can be used in the manufacture of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human vitamin D receptor related (VDKR) polypeptide. Human VDKR polypeptides and substances which affect VDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; vitamin D receptor related protein; VDRR; obesity; diabetes; anorexia; rheumatoid arthritis; lipoprotein detect; hyperlipidaemia; hyperlipoproteinaemia; osteoporosis; tumour:
                                                                                                                                                                                                                                                              Sequence 2802 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New vitamin D receptor related (VDRR) polypeptides, treating obesity, diabetes, anorexia and cheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P PSDB; AAY09516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 OCT 1997;
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                                                                                          276 935B 14 x AAX56243
               1 LendinValArgProLysGiuSerTrpAsnHisAlaAspPheValHisGy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAR : 1998;
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Quality: 2167.
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301 CysGlyArqLeuSerTyrCysLeuGluAspThrAlaGlyGlyPheGlnGl
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TGTGGCCGGCTGTCCTACTGCTTGGAAGACACTGCAGGTGGCTTCCAGCA
                                                                                  GTCAACTGAGATTCAACACAGTGTTCAACGCGGAGACTGGAACCTGGGAG
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                                                                                                      uProlleGluAspGlnHeSerLeuLeuLysGlyAlaAlaPheGluLeur
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seq_documentation_block:
ID AAX78808 standard;
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                          P-PSDB; AAY25411.
                                  WPI; 1999-405024/34.
                                                                                                                                                       W09931129-A1
                                                                                                                                                                                                                                                        nNR7; nNR7-1; nuclear trans-acting receptor protein; human; regulator;
                                                                                                                                                                                                                                                                           Human nNR7-1 cDNA
      DNA encoding human nuclear receptors nNR7
                                                                                                 14-OCT-1998;
                                                                                                                   11-DEC-1998;
                                                                                                                                    24-JUN-1999
                                                                                                                                                                                                                       HOMO
                                                                                                                                                                                                                                                                                              06-SEP-1999
                                                                       (MERI)
                                                                                         12-DEC-1997;
                                                                                                                                                                                                                                                dentification; downstream target gene; cell proliferation;
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97US-0069401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes the isolation of the novel human nuclear receptors nNR7 or nNR7-1. The nNR7 and nNR7-1 proteins are useful in the identification of downstream target genes and ligands regulating its activity. The nuclear receptor is involved in the regulation of in vivo cell proliferation and/or cell development. The nNR7 and nNk7-1 polynucleotides, expression vectors and host cells are useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                             471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2850 BP; 691 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant production of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 28; Fig 4A-C: 80pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnValArgLysAspLeuCysSerLeuLysValSerLeuGlnLeuArgGl
                                                                                                         rHisPheLysAsnPheArgLeuProGlyValLeuSerSerGlyCysGluL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCATGAAACGCAACGCCCGGCTGAGGTGCCCCTTCCGGAAGGGCGCCT
                                                                                                                                                                       LysCysLeuGluSerGlyMetLysLysGluMetIleMetSerAspGluAl
                                                                                                                                                                                                                                                                                                                                                                                                                             GCGAGATCACCCGGAAGACCCGGCGACAGTGCCAGGCCTGCGCCTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9AlaMetLysArqAsnAlaArqLeuArqCysProPheArqLysGlyAlaC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGGACACAGAGTCTGTTCCTGGAAAGCCCAGTGTCAACGCAGATGAGG
                                               euProGluSerLeuGlnAlaProSerArgGluGluAlaAlaLysTrpSer
                                                                                                                                                                                                                                                     CGTGGAGGAGAGGCGGGCCTTGATCAAGCGGAAGAAAAGTGAACGGACAG
                                                                                                                                                                                                                                                                                                                 aValGluGluArqArqAlaLeuIleLysArgLysLysSergluArgThrG
                                                                                                                                                                                                                                                                                                                                                                AAGTGCCTGGAGAUCGGCATGAAGAAGGAGATGATCATGTCCGACGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                            ysGluIleThrArqLysThrArgArgG]nCysG]nAlaCysArqLeuArq
                                                                                                                                                                                                                                        GGACTCAGCCACTGGGAGTGCAGGGGGCTGACAGAGGAGCAGCGGATGATG
Quality:
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5.234
95.392
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Gaps: 1
Percent Identity: 95.392
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seq name: /SIDS8/gcqdata/geneseq/geneseqn/NA1599.DAT:AAX59976
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  Human; intranuclear receptor treatment; ss.
                                                                                                           04 AUG-1999 (first entry)
                                                                                                                                                                                                     AAX59975 Standard; DNA;
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treatment:
                                                                DNA encoding an intranuclear receptor protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ysGluLeuArgPheAsnThrValPheAsnAlaGluThrGlyThrTrpGlu=400
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                                                                                                                                                                                                                                                                                                                                                                   4 1 4
                                                                                                                                                                                                                                                                                                                                                                                                                                 ....PheAlaThr @roLeuMetGluGhiLeuPheGlyHleThrGlyS 414
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                   protein; drug development; diagnosis;
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Homo sapiens

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alignment block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                   Sequence 3057 BP; 792 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be used for the development of drugs and diagnosis and treatment of various diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New intranuclear receptor protein diagnosis and treatment of disease
                               134 LyThrOlmProLeuGlyValGlnGlyLeuThrGluGluGlnArqMetMet 150
                                                                                                                                                 101 f.ysCysLeuGluSerGlyMetf.ysLysGluMetfleMetSerAspGluAl
                                                                                                                                                                                                                                                                                                                                      425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                625 COTOGAGGAGAGGCGGGCCTTGATCAAGCGGAAGAAAAGTGAACGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                       375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 CTGGAGGTGAGACCCAAAGAAAGCTGGAACCATGCTGACTTTGTACACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a human intranuclear receptor protein. The nucleic acid sequence was isolated from a human adult cDNA. Library using a swelltish ANO23 derived probe. The protein can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NISB ) JAPAN TOBACCO
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                                                                                  $61uAspThr61uSerVa1ProGlyLysProSerVa1AsnA1aAsp61u6
GGACTCAGCCACTGGGACTGCAGGGGCTGACAGAGAGGAGCAGCGGATGATG
                                                                                                                                   AAGTGCCTGGAGAGCGGCATGAAGAAGGAGATGATCATGTCCGACGAGGC
                                                                                                                                                                                                                                ysGlulleThrArqLysThrArgArqGluCysGluAlaCysArqLeuArq
                                                                                                                                                                                                                                                                                                     qAlaMetTysArqAsnAlaArqLeuArqCysProPheArqLysGlyAlaC
                                                                                                                                                                                                                                                                                                                                      TATCACTTCAATGTCATGACATGTGAAGGATGCAAGGGCTTTTTTCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Page 35-37; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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Gaps: 1
Percent Identity: 95,492
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                                      414 er 414
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                                                                                                                                                 CGCAGCATCAATGCTCAGCACACCCAGCGGCTGCTGCGCATCCAGGACAT 1524
                                                                                                                                                                                                                                          roAlaHisArgPheLeuPheLeuLysIleMetAlaMetLeuThrGlu... 399
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                                                                         ACACCCCTTTGCTACGCCCCTCATGCAGGAGTTGTTCGGCATCACAGGTA 1574
                                                                                                        .....PheAlaThrProLeuMetGlnGluLeuPheGlyIleThrGlyS 414
                                                                                                                                                                                                                         CTGCTCATAGGTTCTTGTTCCTGAAGATCATGGCTATGCTCACCGAGCTC 1474
                                                                                                                                                                                                                                                                                                                                                                          CCAGACCGCCCAGGTGTGCTGCAGCACCGCGTGGTGGACCAGCTGCAGGA
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alignment_block:
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                                                                                                                           Align seg 1/1
                                                                                                                                                    US-09-276-935B-14 x AAX78807
                                                                                                                                                                                        Ratio: 5.234
Percent Similarity: 95.392
                                                                                                                                                                                                                                                                                         This invention describes the isolation of the novel human nuclear receptors nNR7 or nNR7-1. The nNR7 and nNR7-1 proteins are useful in the identification of downstream target genes and liquids requiation its activity. The nuclear receptor is involved in the requiation of in vivo cell proliferation and/or cell development. The nNR7 and nNR7-1 polynucleotides, expression vectors and host cells are useful for the recombinant production of the protein.
                         422 TGAGGACACAGAGTCTGTTCCTGGAAAGCCCAGTGTCAACGCAGATGAGG 471
                                                                         DNA encoding human nuclear receptors nNR7 and nNR7-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nNR7: nNR7-1; nuclear trans-acting receptor protein; human; identification; downstream target gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Fig 1A-C; 80pp; English.
                                                 17
 4
                                     sGluAspThrGluSerValProGlyLysProSerValAsnAlaAspGlud
luValGlyGlyProGlnIleCysArgValCysGlyAspLysAlaThrGly
                                                                                                                                                                                                                 Quality: 2167.00
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970S-0069401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "nNR7"
/note= "Partial sequence, no start codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
275..1676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   722 COTOGAGGAGAGGGGGGGCTTGATCAAGCGGAAGAAAAGTGAACGGACAG
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seq_documentation_block:
in AAX59974 standard;
              aliqument_scores:
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                                                                                                                      The present sequence encodes a human intranuclear receptor protein. The nucleic acid sequence was isolated from a human adult cDNA library using a swelltish ANO23 derived probe. The protein can
                                                            Sequence 3243 BP; 838
                                                                                         be used for the development of drugs and diagnosis and treatment
of various diseases.
                                                                                                                                                                                  Claim 10: Page 32-35; 38pp; Japanese.
                                                                                                                                                                                                                   diagnosis and treatment of disease
                                                                                                                                                                                                                                  New intrannelear receptor protein - useful for drug development
                                                                                                                                                                                                                                                                P-PSDB; AAY15936
                                                                                                                                                                                                                                                                               WPI: 1999-350330/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; intranuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding an intranuclear receptor protein.
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                                                                                                                                                                                                                                                                                                             (NISB ) JAPAN FOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                       666 [ - AVM - 8 ]
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                                                           862 G; 737
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Ratio: Percent Similarity:

5.234 95.392

Gaps: 1 Percent Identity: 95.392

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGTCCGGAAAGATCTGTGCTCTTTGAAGGTCTCTCTGCAGCTGCGGGG
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seq_name: /SIDS8/qrqdata/qeneseq/geneseqn/NA1999.DAT:AAX56242
                                                                                                                                                                                                                                                                                                                                                                                                                                                _documentation_block:
AAX56242 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1461
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WPI; 1999-302508/25
                                                                                                                                                                                                                                                                   Human: vitamin D receptor related protein: VDRR; obesity; diabetes: anorexia; rheumatoid arthritis; lipoprotein defect: hyporlipidaemia; hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumoni, hyperproliferative skin disorder; hyperthyroidism; ss.
                                                                                                                                                                                                                                                                                                                                                   Human vitamin D receptor related gamma protein encoding cDNA
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                             Berkenstam A,
                                                           (PHAA ) PHARMACIA & UPJOHN
                                                                                             14-OCT-1997;
                                                                                                            31-MAR-1998;
                                                                                                                                           31-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity: 95,172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypoptide. Human VDRR polypoptides and substances which affect VDRR signal transduction, can be used for treating metabolic, proliferative or inflammatory conditions when he was be used in the first form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malign tumours, hyperproliterative skin disorders or hyperthyroidism.
Nucleic acid vectors encoding for expression of a VDRR polypeptide can
be used for treating metabolic, proliferative or inflammatory conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P PSDB; AAY09515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 CTGGAGGTGAGACCCAAAGAAAAGCTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide sequences given in figures 1, 4, 7 and 8, but no figures are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.B. The specification specifically claims the VDRR nucleic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, benign and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or inflammatory conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human vitamin b receptor related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New vitamin D receptor related (VDRR) polypeptides, useful for
treating obesity, diabetes, anorexia and rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ≈
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 TyrHisPheAsnValMetThrCysGluGlyCysLysGlyPhePheArgAr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l landhuValArqProLysGluSerTrpAsnHisAlaAspPheValHisdy
                                                                                                                                                                                                                                                                                                                                                                                                          | InValClyClyProClnHerysArqValCysClyAspLysAlaThrGly 50
lyThrGInProLeuGlyValGlnGlyLeuThrGluGluGlnArgMetMet
                                                                                COTOGAGNAGAGGCGGGCTTGATCAAGCGGAAGAAAAGTGAACGGAACAG
                                                                                                                                                            aValGluGluArqArqAlaLeuTleLysArqLysLysSerGluArqThrG 134
                                                                                                                                                                                                                                                 AAGTGCCTGGAGGGGGGCATGAAGAAGGAGATGATCATGTCCGAGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCCATGAAACGCAACGCCCGGCTGAGGTGCCCCTTCCCGGAAGGGCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qAlaMetLysArgAsnAlaArgLeuArgCysProPheArgLysGlyAlac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGTCGGACGCCCCAAATCTGCCGTGTATGTGGGGACAAGGCCACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOAGGACAGAGTCTGTTCCTTGGAAAGCCCAGTGTCAACGCAGATGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATICACTTCAATGTCATGACATGTGAAAGGATGCAAGGGCTTTTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Page 17-18; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 2151.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 435
Gaps: 2
Percent Identity: 94,943
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1330 CCAGACCGCCCAGGTGTGCTGCAGCACCGCGTGGTGGACCAGCTGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1280 AGCTGCATGAGGAGGAGTATGTGCTGATGCAGGCATCTCCCTCTTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1540 TACACCCCTTTOCTACGCCCCCCATGCAGGAGTTGTTCGGCATCACAGGT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1380 GCAATTCGCCATTACTCTGAAGTCCTACATTGAATGCAATCGGCCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1180 PUTGGCCGGCTGTCCTACTGCTTGGAAGACACTGCAGGTGGCTTCCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1130 GTCAACTGAGATTCAACACAGTGTTCAACGCGGGGAGACTGGAACCTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1080 GCCCATCGAGGACCAGATCTCCCTGCTGAAGGGGGCCGCTTTCGAGCTG1
                                                                                                                                                                                                               1480 CCGCAGCATCAATGCTCAGCAGACCCAGCGGCTGCTGGGGGCATCCAGGACA 1528
414 Ser 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08.8
                                                                                                                                                                                                                                                                                                                                                                                                                          384 roAlaHisArqPheLeuPhe.LeuLysIleMetAlaMetLeuThrGlu..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 PhotysGlytleTleSerPheAlaLysValIleSerTyrPheArqAspto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        880 CAGGTCCGGAAAGATCTGTGCTCTTTGAAGGTCTCTCTGCAGCTGCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 GlnValArqflysAspLeuCysSerLeuLysValSerLeuGlnLeuArqG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 HeArqGlaLeuMetAspAlaGlnMetLysThrPheAspThrThrPheSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                680 GGACTCAGCCACTGGGAGTGCAGGGGCTGACAGAGGAGCAGCGGATGA1G 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 CysGlyArdLeuSerTyrCysLeuGluAspThrAlaGlyGlyPheGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         udJnPheAla1leThrLeuLysSerTyrIleGluCysAsnArqProGlnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUCCAGAGTOTOTOCAGGCCCCATCGAGGGAAGAAGCTGCCAAGTGGAGG
                                                                                                                                                                                                                                                                                                                                                       CTGCTCATAGGTTCTTGTTCCCTGAAGATCATGGCTATGCTCACCGAGCT 1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uProffeGluAspGlnfleSerLeuLeuLysGlyAlaAlaPheGluLeur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACITCTACIGGAGCCCATGCTGAAATTCCACTACATGCTGAAGAAGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....PheAlaThrProteuMetGlnGluLeuPheGlytteThrGly 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        879
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seq_documentation_block:
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an agonist is used where endogenous steroid levels are excessive (e.g. Cushing syndrome; virilism and hirsuitsm in women: polycystic ovarian disease; 11 beta-, 17- or 21-hydroxlase deficiency; 3 beta-hydroxysteroid dehydrogenase deficiency, or breast, colorectal or prostatic cancer), while antagonists are used where endogenous steroid levels are too low. Cells that express SXR are used to identify compounds likely to be involved in undesirable drug interactions. Antibodies specific for SXR are used in immunohistochemical testing for studying distribution/ expression density of SXR, also for diagnosis and therapeutically as
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel nuclear receptor polypeptide, designated SXR (steroid and xenoblotic receptor). SXR (i) forms a heterodimer with retinoid X receptor (RXR), (ii) binds to a direct or inverted repeat response element motif based on the half-site ACTTCA, (iii) activates transcription through response elements present in steroid-inducible P450 genes, in response to a wide variety of natural and synthetic steroid.
                                                                                                                                                                                                       reduce steroid toxicity in subjects being treated with steroids, e.g. in cases of tuberculosis (treated with rifampin and related compounds), breast cancer (treated with tamoxifen, raloxifen etc.) or osteoporosis (treated with Vitamin K), or to slow metabolism of therapeutic steroids. Also, modulating endogenous SXR is used to treat disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                       hormones and (iv) is prominently expressed in liver and intestine. SXR regulates expression of catabolic enzymes, in response to many difference regulates expression of catabolism. SXR is a broad specificity, low-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retinoid X receptor; P450 gene; steroid hormone; steroid metabolism; phytoestrogen; calcium-channel blocker; steroid toxicity; tuberculosis; breast cancer; osteoporosis; Cushing syndrome; virilism; hirsutism;
                                                                                                                                                                                                                                                                                                                       circulation. (Ant)agonists of SXR are used to regulate metabolism of steroids particularly phytoestrogens or calcium-channel blockers, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blumberg B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX89080 standard; DNA; 2068
                                                                                                                                                                                                                                                                                                                                                                      affinity receptor for reducing excessive levels of storoids in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Fig 1A; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           controlling metabolism of steroids and xenobiotics, e.g. reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New steroid and xenobiotic receptor, used to identify modulators for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SALK ) SALK INST BIOLOGICAL STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polycystic ovarian disease; cancer; colorectal; prostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human steroid and xenobiotic receptor (SXR) encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-1999 (first entry)
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/transl_except= (pos:1261..1263, aa:Xaa)
/note= "Xaa= unknown; the start codon is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 583..1887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 steroid and xenobiotic receptor; RXR;
                                                                                                                                                                                                                                                                                                                                                                                                                 in response to many different
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   683 AAGTCGGACGTCCCCAAATCTGCCGTGTATGTGGGGACAAGGCCACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        633 TGAGGACACAGAGTCTGTTCCTGGAAAGCCCAGTGTCAACGCAGAIGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 CTGGAGGTGAGACCCAAAGAAAGCTGGAACCATGCTGACTTTGTACACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2068 BI; 520 A; 541 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding the SXR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          783 GGCCATGAAACGCAACGCCCGGCTGAGGTGCCCCTTCCGGAAGGGCGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 TyrHisPheAsnValMetThrCysGluGlyCysLysGlyPhePhcArqAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 luValGlyGlyProGln1leCysArqValCysGlyAspLysAlaThrGly
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LysGlullePheSerLeuLeuProHisMetAlaAspMetSerThrTyrMe
                                                                                                                                                    GlnValArg1.ysAspLeuCysSerLeuLysValSerLeuGln.LauArgG
                                                                                                                                                                                                                                                                                                         | 11eArgGluLeuMetAspAlaGlnMetLysThrPheAspThrThrPheSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGAGATCACCCGGAAGACCCCGGCGACAGTGCCAGGCCTGCCGCCTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ysGluIlcThrArgLysThrArgArgGlnCysGlnAlaCysArqLeuArg
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                                           GGGAGGATGGCAGTGTCTGGAACTACAAACNCCCAGCCGACAGTGGCCGA
                                                                                                                                CAGGTCCGGAAAGATCTGTGCTCTTTGAAGGTCTCTCTGCAAGCTGCGGG
                                                                                                                                                                                                                                                              euProGluSerLeuGlnAlaProSerArqGluGluAlaAlaLysTrpSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACTCAGCCACTGGGAGTGCAGGGGGCTGACAGAGGAGCAGCGGATGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATCACTTCAATGTCATGACATGTGAAGGATGCAAGGGCTTTTTCAGGAG
                                                                                    lyGluAspGlyScrValTrpAsnTyrLysProProAlaAspSerGlyGly
                                                                                                                                                                                                                    TGCCAGAGCCTCTGCAGGCCCCCATCGAGGGAAGAAGCTGCCAAGTGGAGC
                                                                                                                                                                                                                                                                                                                                                     rHisPheLysAsnPheArgLeuProGlyValLeuSerSerGlyCysGluL
                                                                                                                                                                                                                                                                                                                                                                                              ATCAGGGAGCTGATGGACGCTCAGATGAAAACCTTTGACACTACCTTCTC
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 GIntavillisGIuGIuGIuTyrValLaviMetGInAlaTleSerLavibeSe 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT36499 standard; cDNA; 2191 BF
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   W09622390-A1
                                                                                                                                                                                                                                                                                                                                                                      Xenopus orphan receptor 6 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV 1996 (tirst entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
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                                                                                                                                                                                 Xenopus laevis
                                                                                                                                                                                                                                                                                  hydroxybenzoate;
                                                                                                                                                                                                                                                                                                            Xenopus orphan receptor 6; XOR 6; steroid receptor; vitamin D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCAGCATCAATGCTCAGCACACCCAGCGGCTGCCTGCGGCATCCGAGGACA 1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONGONOATAGGETGTTGTTCONGAAAATGANGGOTATGCNCACCGAGCN 1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPToASpArqPToG1yVa1LeuG1nHisArqVa1Va1AspG1nLeuG1nG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCTGCATGAGGAGGAGTATGTGCTGATGCAGGCCATCTCCCCTCTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACTTCTACTGGAGGCCATGCTGAAATTCCACTIACATGCTGAAGAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InfentententhurroMettentysPheHisTyrMettentystysLen 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....PhoAlaThrProLeuMotGluGluLouPhoGlyIloThrGly 413
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167..1827
/*Lag a
                                                                                                                                                                                                                                                                            mercaptobenzoate; aminobenzoate; transcription;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignmeut_block:
US-09-276-9358 14 x AAT36499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aliqument_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 910.50
Ratio: 4.129
Percent Similarity: 69.952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seq 1/1 to: AAT36499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The cDNA can be used for produ. of recombinant XOR-6 in animal host cells and as a probe to determine tissue XOR-6 mRNA levels as a means of assessing sensitivity to e.g. amino benzoates (used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed nuclear hormone receptors; 3 clones were identified from an eag cDNA library and 2 from a dorsal blastopore lip cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AAR98521), a new member of the steroid receptor superfamily, characterised as being responsive to the presence of hydroxy, mercapto or amino benzoate(s) and as regulating the transcription of associated gene(s). It was identified in a screen to maternally.
                                                                503 OTOGAACAGAGAGGAGCGCTAATTAAGAGAAAAACACAAATTAACGAAATT
                                                                                                                          18
                                                                                                                                                                                                                                                  <u>-</u>
                                                                                                                                                                                                                                                                                                            403 COTCATCAACAAGAGCAATCGGCGCCACTGCCAGGCCTGTCGGCTCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                          356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 ATCACTTCAATGCTATGACCTGCGAGGGCTGCAAGGGATTCTTCAGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 GAGGAGGAAGAAGACGCCTCTAACAGTTGTGGGACGGGGGAAGACGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2191 BP; 551 A; 526 C; 605 G; 509 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sunscreens).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A cDNA clone (AAT36499) codes for Xenopus orphan receptor 6 (XOR-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 24-26; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding receptor polypeptide responsive to hydroxy, mercapto or amino benzoate(s) - useful to regulate gene transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blumberg B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SALK ) SALK INST BIOLOGICAL STUDIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 - JBIU - 1596
                                                                                                                                                                                                                                                                                                                                                                             34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5) yrHisPheAsnValMetThrCysGluGlyCysLysGlyPhePheArqArq 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 GluAspThrGluSerValProGlyLysProSerValAsnAlaAspGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaMetLysArqAsnAlaArqLeuArqCysProPheArqLysGlyAlaCy
rGlyThrGInProLeuGlyValGlnGlyLeuThrGluGluGlnArqMetM
                                                                                       ValGluGluArqArqAlaLeuIlelysArqLys...LysSerGluArqTh 133
                                                                                                                                                                                                                     ystysiawdiuserGlyMetLystysGluMet.HeMetSerAspGluAla 117
                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGTGAAGAGGAACTTGCGGCTCAGCTGCCCCTTC...CAGAATTCCTG
                                                                                                                                                                                                                                                                                                                                                                   sGlutleThrArgLysThrArgArgGlnCysGlnAlaCysArgLeuArgL 101
                                                                                                                                                                                     ANTIGTICT GGACATCIGGCATGAGGAGAGAGTTGATCATGTCCGATGCAGGG
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Gaps: 10
Percent Identity: 46.154
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seq_name:
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                                                             1268 TGGGACATTCAGCCTGATGCCACCCCACTTATGCGAGAAGTCTTTGGA 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          671
                                                                                                                                                                                                                                                                                                                                                                                                  etPheLysGlyIleIleSerPheAlaLysValIleSerTyrPheArgAsp 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICTCACTCAACTGGTTGGGGCCCACACCCAAAACCTTTGACTTCAACTTC
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                                                                                                                                                                          CAGAGCTTCGGACAGCAATGACATACACAGCAGCAGCTCCTGGAGATC 1267
                                                                                                                                                                                                                                                                                         CCCCTCCCGCAGAACAGGCTCCTGTACeCCAAGATCATGGAGTGTCTGA 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnGluGlnPheAlaIleThrLeuLysSerTyrfleGluCysAsnArg.. 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heSerProAspArgProGlyValLeuGlnHisArgValValAspGlnLeu 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTCAGCTGTTCCTGGAGCCCCCTGGTGAGGATTCATCGCATGATGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnGlnLeuLeuGluProMetLeuLysPheHisTyrMetLeuLysLy 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTIGTGGCCCCTTCACCTATGACACTGAGGATATGTTCCTGGCCGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               luCysGlyArgLeuSerTyrCysLeuGluAspThr...AlaGlyGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCTGTGATCCGATTCAACACTGTGTTTAACTCTGACACCAATACGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uCysGlnLeuArgPheAsnThrValPheAsnAlaGluThrGlyThrTrpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGACATTGAAGACCAAATTGCTCTCCTGAAAGGTTCTGTAGCGGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuProIleGluAspGlnIleSerf.euf.euf.ysGlyAlaAlaPheGluLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATCAAGGGCATCATCAGCTTTGCCAAAATGCTCCCCTACTTCAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yLysGlullePheSerLeuLeuProHisMetAlaAspMetSerThrTyrM 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTCAGACCCAACT.....CAGGAGCCCCAAGCCACCTCT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyGluAspGlySerValTrpAsnTyrLysProProAlaAspSerGlyGl 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erGlnValArgLysAspLeuCysSerLeuLysValSerLeuGlnLeuArg 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uLeuProGluSerLeuGlnAlaProSerArgGluGluAlaAlaLysTrpS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTTCTCCAAGAACTTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerHisPheLysAsnPheArgLeuProGlyValLeuSerSerGlyCysGl 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        etileArgGluLeuMetAspAlaGlnMctLysThrPheAspThrThrPhe 166
                                                                                                                                                                                                                              hrGluPhe ..... 400
                                                                                                                                                                                                                                                                                                                                              .ProGlnProAlaHisArgPheLeuPheLeuLysIleMetAlaMetLeuT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGCTTCTTACCGACCGGGGGTCTGCGACTGGGAGAAGATCCAGAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGAATGTACAGAGTGAGGAATACGCCATGATGGCCGCTCTCTCCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .TCTGAAGCCTTTTTGATGCTACCTCATATATCTGACCTCGTTACCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ......AGA
/SIDS8/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV03129
                                                                                                                  .....AlaThrProLeuMetGlnGluLeuPheGly 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAATAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             967
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alignment_block:
US-09-276-935B-14 x AAV03129
                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID AAV03129 standard; cDNA; 1960
                                                                                                                                                                                                                                       alignment_scores
                                                                                                                   Align seg 1/1 to: AAV03129 from: 1 to: 1960
                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                         A novel cDNA sequence encodes the rat vitamin D receptor isoform protein (VDR1). The isoform differs from the normal receptor (VDR0), which is encoded by the present sequence, in having the vitamin D response element curtailed by 86 residues, and having an extra 19 residues inserted at the C-terminal of this element. It extra as a dominant negative receptor in the vitamin D signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 46pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding a vitamin D receptor isoform protein - useful for bone density determination and for screening substances for vitamin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-051917/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9747172-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dominant negative receptor; signal transmission channel; bone density disorder; screening; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding rat vitamin D receptor (VDRO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1998
                                                                                                                                                                                                                                                                                    Sequence 1960 BP; 432 A;
                                                                                                                                                                                                                                                                                                                                              transmission channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW47509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kato S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHUS ) CHUGAI PHARM CO LTD (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; vitamin D receptor; isoform protein; VDR1; VDR0; diagnosis;
            38 ProGinIleCysArgValCysGlyAspLysAlaThrGlyTyrHisPheAs 54
                                                                                                                                                                                                                                                                                                             isoform protein can be used to diagnose bone density disorders screen for substances having potential vitamin \text{D-like} activity
TGCTATGACCTGTGAAGGCTGCAAAGGTTTCTTCAGGCGGAGCATGAAGC
                                                           CCCCGGATCTGTGGAGTGTGTGGAGACCGAGCCACAGGCTTCCACTTCAA
                                                                                                                                                                                                                       Ouality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ueno K;
                                                                                                                                                                                                            Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96JP-0194179
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                                                                                                                                                                                             762.00
2.712
68.537
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12..1283
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                                                                                                                                                                                                                                                                                    620 C; 497 G; 411 T; U other;
                                                                                                                                                                                      Length: 410
Caps: 8
Percent Identity: 40.000
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789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219
۲۰, ۶
                                                                                                                                                                                              939 ATAAAGTTCCAGGTGGGGGCTGAAGAAGCTGAACTTACATGAGGAAGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B FF CATGGATGATATGTCCTGGGACTGTGGCAGCCAGGGACTACAAGTACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 tAlaAspMetSerThrTyrMetPheLysGlyllelleSerPheAlaLysV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 uMotAspAlaGlnMotLysThrPhoAspThrThrPhoSorHisPhoLysA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 AGAGGGAGATGATAATGAAGAGAAAAGAGGAAGAGGCCTTGAAGGACAGT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 CATCOCCATGATGAAGGAGTFCATCCTGACAGAGTGAGGAGGTACAGCGTA
                                                                                                                     440 rValleuMetGlnAlalleSerLeuPheSerProAspArgProGlyValL 357
                                                                                                                                                                                                                                                            324 LeubysPheHisTyrMetLeubysLysLeuGlaLeuHisGlaGlaGlaTy
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                                                                                                                                                                                                                                                                                                                                 TCACCGATGICTICCAAAGCTGGGCACACCCTGGAGCTGATCGAGCCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgArgAlaLeufleLysArghysLysSerdTuArgThrGlyThrGlnPro 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgLysThrArgArgGInCysGInAlaCysArgLeuArgLysCysLeuGl 104
                                                                 spThr.....AlaGlyGlyPheGlnGlnLeuLeuGluProMet 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nAlaGluThrGlyThrTrpGluCysGlyArgLeuSerTyrCysLeuGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LyselyAlaAlaPheeluLeuCyseInLeuArgPheAsnThrValPheAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTGACCTTGTCAGTTACAGGATCGAAAAAGGTCATCGGCTTTGGCCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACCCGTCTGTGACTCTGGACCTGTCTCTCTCTCTCTGCATGCTGCCCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProProAlaAspSerGlyGlyLysGluIlePheSerLeuLeuProHisMe 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluSerLeuGlnAlaProSerArqGluGluAlaAlaLysTrpSerGlnVa 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTITICCGGCCTCCCAGTITCGTATGGACGGAAGTFACAGGGAGCTATTCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GETGRIAGGCCACCACAAGACCTATGACCCCACCTACGCTGACTTCAGGG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAGGCCCAAG...CTATCTGAAGAAGAAGAAGCACATCATAGCCATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aSerGlyMetLysLysGluMetTleMetSerAspGluAlaValGluGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAGGCCCGGTTCACCGGTCCCCTTC...AATGGAGATTGCCCGCATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGT CAAGCCCATTGAGGTGATCATGTTACGCTCCAACCAGTCTTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....SerLeuGluLeuArqGlyGluAspGlySerValTrpAsnTyrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGACAACCGGCGACACTGCCCAGGCCTGCCGGGCTCAAACGCTGTGTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....CCCACACTCAGCTTCTCCGGGAACTCCTCCTCCTCC 553
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171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS8/qcqdata/qeneseq/qeneseqn/NA1993.DAT:AAQ51425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1239 CTCACACCCCTTGTGCTGGAGGTGTTCGGC 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1189 ACTECAAACAATACCGCTCCCCTCCTCCTTCCAGCCCGAGAATAGCATGAAG 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1039 AGGACGCCAAGCTGGTGGAAGCCATTCAGGACCGCCTATCCAACACGCTG
                         using insect host cells transformed with DNA coding for an animal (pret human, rat, porcine or avian) vitamin b receptor. The coding sequence is incorporated into a recombinant baculovirus vector for transformation of the insect host. The rat version of the coding sequence was published in Burmester et al., Proc.Natl. Acad.Sci USA 85:9499-9502 (1988).
                                                                                                                                                                                           Recombinant product of 1,25-dichydroxy-vitamin by receptor using expression system comprising insect cell host and recombinant virus contg. foreign DNA
                                                                                                                                                           Disclosure; Columns 15-18; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 AlaThrProLouMetGlnGluLeuPheGly 410
Sequence 204 ( BP; 448 A; 647 C; 518 G; 430
                                                                                                                            The 1,25-dihydroxyvitamin D3 receptor is recombinantly produced
                                                                                                                                                                                                                                                            P-PSDB: AAK43656
                                                                                                                                                                                                                                                                            WPT: 1993-367874/46.
                                                                                                                                                                                                                                                                                                                                            (WISC ) WISCONSIN ALUMNI RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5260199-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insect host; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.25 dihydroxyvitamin D3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat vitamin D receptor coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ51425 standard; cDNA; 2043 BP
                                                                                                                                                                                                                                                                                                                                                                            30 - .101, - 1551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eLeuLys1}eMetAlaMetLeuThrGluPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCAAGATGATCCAGAAACTGGCCGACCTGCGGAGCCTCAACGAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysSerTyrlleCluCysAsnArgProGlnProAlaHisArgPheLenPh
                                                                                                                                                                                                                                                                                                             ΞF,
                                                                                                                                                                                                                                                                                                            Prahi JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                            9108-0737736
                                                                                                                                                                                                                                                                                                                                                                                                            9108-0737736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
266...1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= vitamin_D_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*t.ag=
                                                                                                                                                                                                                                                                                                            ROSS TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor; recombinant protein production
T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400
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                                                                                                                                                                                                                           protein
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aliqument_scores

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alignment_block:
US-09-276-935B-14 x AAQ51425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452
                                                     277 LysGlyAlaAlaPheGluLeuCysGlnLeuArgPheAsnThrValPheAs 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 lArqLysAspLeuCysSerLeuLysVal...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 snPheArqLeuProGlyValLeu.....SerSerGlyCysGluLeuPro 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 uMetAspAlaGlnMetLysThrPheAspThrThrPheSerHisPheLysA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 CATCGCCATGATGAAGGAGTTCATCCTGACAGATGAGGAGGTACAGCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 ProGlnileCysArgValCysGlyAspLysAlaThrGlyTyrHisPheAs 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGGACAACCGGCGACACTGCCAGGCCTGCCGGCTCAAACGCTGTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rgAsnAlaArgLeuArgCysProPheArgLysGlyAlaCysGluIleThr 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCGGATCTGTGGAGTGTGTGGAGACCGAGCCACAGGCTTCCACTTCAA
                                                                                                                                                                 allleSerTyrPheArgAspLeuProIleGluAspGlnIleSerLeuLeu
                                                                                                                                                                                                                                                                                                                                                               GACCCGTCTGTGACTCTGGACCTGTCTCTCTCTCCATGCTGCCCCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCTCTGACCTGTACACCACCTCACTAGACATGATGGAACCATCCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluSerLeuGlnAlaProSerArgGluGluAlaAlaLysTrpSerGlnVa 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAGGCCCAAG...CTATCTGAAGAACAACAGCACATCATAGCCATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uSerGlyMetLysLysGluMetIleMetSerAspGluAlaValGluGluA 121
AAGTCAAGCGCCATTGAGGTGATCATGTTACGCTCCAACCAGTCTTTCAC
                                                                                                                     TGATCCCAGGATTCAGGGATCTCACCTCCGATGACCAGATTGTCCTGCTT
                                                                                                                                                                                                                                             GGCTGACCTTGTCAGTTACAGCATCCAAAAGGTCATCGGCTTTGCCAAGA
                                                                                                                                                                                                                                                                                                   tAlaAspMetSerThrTyrMetPheLysClyIleIleSerPheAlaLysV
                                                                                                                                                                                                                                                                                                                                                                                                                        ProProAlaAspSerGlyGlyLysGluIlePheSerLeuLeuProHisMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTCCAACCTGGATCTGAACGGAGAGGATTCTGAT........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGGACGCCCACCACAAGACCTATGACCCCACCTACGCTGACTTCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuGlyValGlnGlyLeuThrGluGluGlnArgMetMetIleArgGluLe 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGGGAGATGATAATGAAGAGAAAAAGAGGAAGAGGACCTTGAAGGACAGT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rgArgAlaLeuIleLysArgLysLysSerGluArgThrGlyThrGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgLysThrArgArgGlnCysGlnAlaCysArgLeuArgLysCysLeuGl 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCTATGACCTGTGAAGGCTGCAAAGGTTTCTTCAGGCGGAGCATGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ....SerteuGlnLeuArgGlyGluAspGlySerValTrpAsnTyrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGG..........CCCACACTCAGCTTCTCCGGGGAACTCCTCCTCC 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTTCCGGCCTCCAGTTCGTATGGACGGAAGTACAGGGAGCTATTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     762.00
2.712
68.537
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92]
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                                                                                                                     871
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seq_documentation_block:
ID AAX34789 standard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1322 CTCACACCCCTTGTGCTGGAGGTGTTCGGC 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1272 ACTCCAAACAATACCGCTCCCTCTCCTTCCAGCCCGAGAATAGCATGAAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1022 ATAAAGTTCCAGGTGGGGCTGAAGAAGCTGAACTTACATGAGGAAGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         972 TEACCGATGTCTCCAAAGCTGGGCACCCCTGGAGCTGATCGAGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 LeuLysPheHisTyrMetLeuLysLysLeuGlnLeuHisGluGluGluTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         922 CATGGATGATATGTCCTGGGACTGTGGCAGCCAGGACTACAAGTACGACG
                                                                      D receptor or variant transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of human vitamin D receptor (VDR) gene transcript 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX34789 standard; DNA; 1382 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 AlaThrProLeuMetGlnGluLeuPheGly 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 euGlnHisArgValValAspGlnLeuGlnGluGlnPheAlaIleThrLeu 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 spThr.....AlaGlyGlyPheGInGInLeuLeuGhuProMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 nAlaGluThrGlyThrTrpGluCysGlyArqLeuSerTyrCysLeuGluA 310
                                                                                        New polynucleotides which encode novel isoforms of the human vitamin
                                                                                                                                                    WPI; 1999-263693/22.
                                                                                                                                                                                          Crofts LA,
                                                                                                                                                                                                                            (GARV-) GARVAN INST MEDICAL RES
                                                                                                                                                                                                                                                                  29-SEP-1997;
                                                                                                                                                                                                                                                                                                        29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                              08-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                  W09916872-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vitamin D receptor; VDR; hVDR; variant; isoform; SRC-1; GRIP-1; TF11H: cofactor; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rValLeuMetGlnAlaIleSerLeuPheSerProAspArgProGlyValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCAAGATGATCCAGAAACTGGCCGACCTGCGGAGCCTCAACGAGGAAC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysSerTyrlleGluCysAsnArgProGlnProAlaHisArgPheLeuPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eLeuLysIlcMetAlaMetLeuThrGluPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGACCTACATCCGCTGCCGCCACCCGCCCCCAGGCAGCCACCAGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGACGCCAAGCTGGTGGAAGCCATTCAGGACCGCCTATCCAACACGCTG
                                                                                                                                                                                        Eisman JA,
                                                                                                                                                                                                                                                                    97AU-0009500
                                                                                                                                                                                                                                                                                                        98W0-AU00817
                                                                                                                                                                                          Hancock MS,
                                                                      for
                                                                                                                                                                                          Morrison
                                                                        hVDR
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The invention relates to isolated polynucleotides which encode novel

Claim 4; Fig 6; 56pp; English

% 88888888888

aliqument_block: alignment, scores: Ratio: 2.688 Percent Similarity: 67.718 Aliqu seq 1/1 to: AAX34789 from: 1 to: 1882 09 276 935B-14 x AAX34789 isotorms of the human vitamin b receptor (VDR) or variant transcripts for hVDR. The polynucleotides are useful in methods for detecting agonist and /or antagonist compound of a VDR isotorm. An increase or decrease in activity of the receptor may be detected by measuring changes in interactions with known cofactors (e.g. sRC-1, GRTP-1 and TETID) or unknown cofactors (e.g. through use of the dual hybrid system). The polynucleotides shown in AAX4787, AAX4791 and AAX4792 (corresponding polynucleotides shown in AAX4787, AAX4791 and AAX4792 (corresponding to hVDM exon sequences) may be useful as probes for the detection of VDM variant transcripts and for assessing cell or tissue specific expression of variant transcripts. The present sequence represents the nucleotide 697 CCAGCTTCTCCAATCTGGATCTGAGTGAAGAAGATTCAGAT..... 208 erlædlysValSerlædInLeuArgGlyGluAspGlySerValTrpAsn 224 171 snPheArgLeuProGlyVallauSerSerGly......cysGlu 183 4.56 406 104 306 159 CCCCGGATCTGTGGGGGTGTGTGGAGACCGAGCCACTGGCTTTCACTTCAA 647 CTCCTCTCACATCACTCTATCACCTCTTCAGACATGATGGACTCGT 603 AGGCCCAACTECCAGACACACTCCCAGC.....TTCTCTCTGGGGACTCCTC 646 184 LeuProGluSerLeuGlnAlaProSerArqGluGluAlaAlaLysTrpSe 200 553 ACTICOUNCERCACTICOTGANICATGATGATGAGGAGGAACCTICC 138 LeuclyValGlnGlyLeuThrGluGlnGlnArqMetMet1leArgGluLe 154 121 rqArqAlaLeuHehysArqbyshysSerGluArqThrGlyThrGluPro 137 556 CATCGGCATGATGAAGGAGTTCATTCTGACAGATGAGGAAGTGCAGAGGA 405 Sequence 1382 BP; 310 A; 409 C; 379 G; 284 T; 0 other; sequence of hVDR gene transcript 9. 209 FGCTATGACCTGTGAAGGCTGCAAAGGCTTCTTCAGGCGAAGCATGAAGC 88 71 rqAsnAlaArqLeuArqCysProPheArqLysGlyAlaCysGlulleThr 87 54 nValMetThrCysGluGlyCysLysGlyPhePheArgArgAlaMetLysA 71 uSerGlyMetLysLysGluMetileMetSerAspGluAlaValGluGluA 121 ArqLysThrArqArqGInCysGInAlaCysArqLouArqLysCysLeuGl 104 GGAAGGCACTATTCACCTGCCCCTTC...AACGGGGACTGCCGCATCACC CTGCGGCCCAAG...,CTGTCTGAGGAGCAGCAGCGCATCATTGCCATACT ACCCCCACATGATTCCTGAAGCGGAAGGAGGAGGAGGGCTTTGAAGGACACT 455 AAGGACAACGGACGCCACTGCCAGGCCTGCCGGCTCAAACGCTGTGTGGA Quality: 750.00 Percent Identity: 40.291 Length: Gabs: 355

	ATGAAGCTAAGGCCCCTTGTGCTCGAAGTGTTTGGC 1367	1332
	AlaThrProLeuMetGlnGinLeuPheGly 410	401
1331	AGGAGEACTCCAAGEAGTACCOCTGCCTCTCCTTCCAGCCTGAGTGCAGC	1282
400		400
1281	eneuPheteulysTicMetAlaMetLeuBhrGluPhe	1232
1231	+-7	1182
388	35	372
1181	Ö	1132
371	110	355
455 1131	udintyrvalleumetolinalallesorteuphosproproprakraprod 	1082
1081	COCOCATOAGTTCCAGTGGGACTGAAGAAGCTGAACTTGCATGAGGA	1032
38	ProMetLeuLysPheHisTyrMetLeuLysLysLeuGlnLeuHisGluGl	322
1041	ACCOCOTCACTGACGTGACCAAAGCCGGACACACCCTGGAGCTGATTGAC	982
121		307
981	CIPCACCATGUACGACATGTCCTGGACCTGTGGCAACCAAGACTACAAGT	942
406		16.7
931	CIGCTGANGTCAAGTGCCATTGAGGTCATCATGTTGCGCTCCAAIGAGTC	882
291		275
881	CTAAGATGATACCAGGATTCAGAGACCTCAGCTCTGAGGACCAGATGGTA	832
274	laLysVallleSerTyrPheArqAspLeuProlleGluAspGlnlleSer	258
831	CCACCTGGCTGACCTGGTCAGTTACAGCATCCAAAAGGTCATTGGCTTTG	782
84.7		241
781	GACCCTTCTGTGACCCTAGAGCTGTCCCAGGTCTCCAFGCTGCC	738
241		225

Thu Jul 12 14:23:34 2001

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Database sequences: 10228115
Database length: 431459454
Search time (sec): 1360.0000
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qb_est48:AW511148
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gb_est29:AL555760
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gb_est43:AW158294
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AK018630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                     Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
                                                                                                                                                                                                                                                                        Direct Submission Submitted (10-JUL-2000) Yoshibide Hayashizaki. The Institute of
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further details
                         Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yo
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.rikon.go.jp.
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5 (bases 1 to 2525)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The RIKEN Genome Exploration Research Group Phase II Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci, P. and Hayashizaki, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
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                                                                     Fax:81-45-503-9216)
                                                                                               URL:http://genome.gsc.riken.go.jp/, Tel:81 45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FANTOM Consortium
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Sciurognathi; Muridae; Murinae; Mus
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AV652654 AV652753 GLC Homo s
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cDNA library was prepared and sequenced in Encyclopedia Project of Genome Exploration Genomic Sciences Center and Genome Science

Mouse Genome Research Group

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alignment block:
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                                                                                       qAlaMetLysArgAsnAlaArgteuArgCysProPheArgLysGLyAlac
GGCATGAAACGCAATGTCCCGGCTGAGGTGCCCCCTTCCCGAAGGGAACCT
                                                                                                                                                                                                 TyrHisPhoAsnValMetThrCysGluGlyCysLysGlyPhoPhoArgAr 67
                                                                                                                                                        TALCACTTCAATGTCATGACGTGTGAAGGATGCAAGGGGTTTTTTCAGAAG
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TWNVQPPSKSDSKEITPLLPHLADVSTYMEKGVINEAKVISYVRDLPIEDQISILLKGA
TEEM
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/db_xref-"GH-128-84-85"
/db_xref-"GH-128-84-85"
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/translation="mkeesswsrvglvg/gebadsaleepinveesdogloickrolkkcles
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gmkkemimsdaaveggraalikkkkkeekieapppkggglitebogaligelmdagmgffd
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/clone_lib="RIKEN_tull-length enriched mouse cDNA_library"
/dev_stage:"adult"
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/db_xret~"MGD:MG1:1897757"
/ctone~"9130016118"
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/codon_start=1
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/db_xref="taxon:10090"
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CTGCTCACAGGTTCCTGTTCCTGAAGATCATGGCCGTCCTCACTGAGCTG
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                           Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :, mRNA sequence.
AI746915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia: Eutheria;
l (bases 1 to 794)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI746915.1 GI:5125179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer: custom primer used
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314 286 1810
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                                                                                                                                                                                                                Custom primers for sequencing: 5' end CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                            [TGTTGGCCTACTGG], digested and cloned into distinct Draili sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT];
  610.50
4.424
88.462
                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded cDNA was ligated to a DraIII adaptor
                                                                                                                                                                                                                                                             insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib-"Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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Percent Identity: 74.359
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REFERENCE
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US-09-276-935B-14 x AI746915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qh77b12.x1 Soares fetal_liver_spleen_lnFLS_S1 Homo clone IMAGE:1850687 3' similar to gb:J03258 VITAMIN (HUMAN);, mRNA seguence
                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cqapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                            EST
                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMAN):, mRNA sequence.
A1248626
A1248626.1 GI:3844023
                                      Insert Length: 608 Std Erro
Seq primer: -40UP from Gibco
                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                   1 (bases 1 to 343)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicqap
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                  High quality sequence stop: 338
                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                    Tumor Gene Index
                                                                                                                                                                                                                                              National Cancer Institute, Cancer
                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Location/Qualifiers
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG FGCCTGGAGAGCGGC 1
                                                                                                                                                                                                                                                                                            AKO11108 677 bp mRNA HTC 08-FEB-2001 Mus masculus 13 days embryo liver cDNA, RIKEN toll length enriched library, clone:2510047b01, bill insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                           Mus musculus (strain:65/BL/6J) lidays embryo liver cDNA to mRNA, clone_lib:RTKEN tuli length curiched mouse cDNA library
                                                                                                                                        CVE Frabber
cloue: 2510047b01
                                                                                                                                                                                                          AK011108.1 G1:12847017
                                                                                                                                                                                                                                                           AKO11108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constructed by Bento Soates and M.Fatima Bonaldo."
108 c 93 q 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note "Organ: Liver and Spicen: Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac 1: Site_2: Eco RI: This is a subtracted version of the original Soares tetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         went through one round of normalization. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Eco RI sites of the modified pT213 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver spleen INFLS library. Ist strand dDNA was primed with a Pac i - oliqu(dP) primer [5]
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/Tab_host "DHTOB (ampleTHTIn resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib-"Soares_tetal_liver_spleen_lNFLS_Sl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism "Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.614
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COMMENT
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                                                                         SOHECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Banaqaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiracka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihata, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Cwa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shihata, K., Shihata, Y., Taqawa, A., Takahashi, F., Yamamura, T., Yasunishi, A., Yoshino, M., Maramatsu, M., and Hayashizaki, Y., Voshida, K., Yoshino, M., Maramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kashiwaqi,K., Fujiwake,S., Inoue,K., Toqawa,Y., Izawa,M., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                               prepared by using trebalose thermo-activated reverse transcriptuse and subsequently enriched for full-length by cap trapper, CDNA went through one round of normalization to Rot 5.0 and subtraction to
                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://denome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                URL:http://genomo.gsc.riken.go.jp/, Tcl:81-45-503-9222)
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
RIKEN Yokohama Institute: 1–7–22 Suehiro ebo, Tsurumi-ku, Yokohama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409,
5 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kikuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A., Yamamoto, R., Matsumoto, H., Sakaquchi, S., Ikoqami, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata.K., Itoh,M., Aizawa.K., Nagaoka.S.
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20499374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carpinci, P., Shibata, Y., Hayatsu, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High-efficiency full-length cDNA cloning Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninei, P. and Hayashizaki, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
                                                                                                                                                                                     with Xhol and Sstl. Cloning sites,
                                                                                                                                                                                                                                                                      of sequence (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kanaqawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FANTOM Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase II leam and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20530913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 677)
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                                                                                                                                                                                                                                                                                                    25.0. Second strand cDNA was prepared with the primer adapted
/strain "C57BL/6J"
                                          /organism-"Mus musculus"
                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagaoka, S., Sasaki, N., Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inome, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Tashiro.H., Itoh,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Izawa, M., Ohara, E.,
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seq_name: gb_est31:AU140214
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                                                                                                                     KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                          aValGluGluArgArgAlaLeuIleLysArg 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ysGluIleThrArgLysThrArgArgGlnCysGlnAlaCysArgLeuArg 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGAGATCACCCGGAAGACACGACGGCAGTGCCAGGCCTGCCGTTTGCGC 595
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 837)
                                                                                                                                                                                                   AU140214 837 bp mRNA EST 25-OCT-2000 AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="13 days embryo"
305. .>677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 CCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTCACTTCAA
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                                                                                                                                                                                                                                                                                                                                                                 uSerGlyMctLysLysGluMetIleMetSerAspGluAlaValGluGluA 121
                                                  GCTGGACGCCCACCATAAGACCTACGACCCCACCTACTCCGACTTCTGCC 400
                                                                                                                                              CTGCGGCCCAAG...CTGTCTGAGGAGCAGCAGCAGCATCATTGCCATACT
                                                                                                                                                                                                                                           AGCGGGAGATGATCCTGAAGCGGAAGGAGGAGGAGGAGGCCTTGAAGGACAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAGGCACTATTCACCTGCCCCTTC...AACGGGGACTGCCGCATCACC 153
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                                                                                            uMetAspAlaGlnMetLysThrPheAspThrThrPheSerHisPheLysA 171
                                                                                                                                                                                           LeuGlyValGlnGlyLeuThrGluGlnArgMetMetIleArqGluLe
                                                                                                                                                                                                                                                                                                                                          CATCGGCATGATGAAGGAGTTCATTCTGACAGATGAGGAAGTGCAGAGGA
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Ratio:
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Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genomics&hri.co.jp

BRI human cDNA project; 5'-& 3'-end one pass sequencing: Heiix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.
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1532-4 Yana, Kisarazu, Chiba 292-0812,
Tel: 81-438-52-3951
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71.071
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                                   SOULCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW871811 493 bp mrna EST 40-MAR 2001 da94c06.yl Xenopus laevis tadpole stage 24 Xenopus laevis cDNA 5' similar to qb:J03258 VITAMIN D3 RECEPTOR (HUMAN);, mrna sequence.
                                                                                                                                                                                                                                   Washington University Genome Sequencing Center
Clone distribution: Xemopus clones from this library are available
                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Nox 8501, St. Lonis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Huderwood,K., Theising,B., Bowers,Y., Person,JR., Gibbons,M., Harvey,M., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metuzoa: Chordata: Cianiata: Vertebrata: Enteleostomi;
Amphibia: Batrachia: Anura: Mesobatrachia: Pipoidea: Pipidae:
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                                                                                                High quality sequence stop: 418
                                                                                                                                       Seq primer: 40RP trom Gibeo
                                                                                                                                                                       address: www.izpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU Kenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Sandy Clitton, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olher_ESTs: da94c06.xl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU Xenopus EST project, 1999
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                                                                                                                                                                                                   through the RessourcenZentrumPrimarDatenbank, Berlin, Germany (web
                                                                                                                                                                                                                                                                                                           Library constructed by B. Korn PhD. and S. Henze DNA Sequencing by:
                                                                                                                                                                                                                                                                                                                                              Email: estawatson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 414 286 1800
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Zorganism "Xemopus laevis"
                                                            Location/Qualitiers
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                 seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 FCAGGCGGGCGTGAAGAGGAACTTGCGGCTCAGCTGCCCCCTTC...CAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 heArdArdAlaMetLysArdAsnAlaArdLeuArdCysProPheArdLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 CACTGGGTATCACTTCAATGCTATGACCTGCGAGGGCTGCAAGGGATTCT 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt 12.AspGluGluValGlyGlyProGlntleCysArqValCysGlyAspLysAl}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qMetMetTleArqGluLeuMetAspAlaGlnMetLysThrPheAspThrT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp@1uAlaValGluGluArqArqAlaLeuIleLysArqlysLysSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACTITICICACTCAACTGGTTGGGGGCCACACACCAAAACCTTTGACTTCA
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                                                                                                                                                                                                                                                                                                                                                                                          ACT TO ACCUTE CTC CAAGAACTTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArqThrGlyThrGlnProLeuGlyVa1GlnGlyLeuThrGluGlnGlnAr 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCAGCGGTGGAACAGAGAGAGGGCGCTAATTAAGAGAAAACACAAATTA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qLeuArqLysCysLeuGluSerGlyMctLysLysGluMctlleMetSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library, clone:0610010018, full insert sequence AK002513
                                                                                                                                                                                                      AKO02513 1728 bp. mkNA HTC 08-FEB-2003
Mus musculus adult mate kidney cDNA, RIKEN 1911 length enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                        Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mkNA, clone_lib:RIKEN_full-length_enriched_mouse_cDNA_libiary
clone:0610010018
                                                                                CAP trappet.
                                                                                                               AK002514.1 GI:12842549
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/note."Vector: prWvSpokTb; Site_1: Not1: Site_2: Sall:
/note."Vector: prWvSpokTb; Site_1: Not1: Site_2: Sall:
Method of cloning used: directed liquation: insert:heek:
95.8 blue and 4.2 white. Library constructed by Jr.
85.8 blue and Sabine Henze. Note: This is a Xenopus
Gene Collection (XGC) library."
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/dev_stage="stage 24"
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/sex "mixed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adachi, Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Haraka, A., Hayatsu, N., Hirmoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, M., Nishi, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, M., Nishi, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, M., Nishi, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Kitkuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Kikuchi,N., Yamamoto,R., Matsumoto,H., Sakayuchi,S., Ikegami,T., Harada,A., Yamamoto,R., Matsuncto,H., Sakayuchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Toqawa,Y., Izawa,M., Ohara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunra,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanadawa 230-0045, Japan (E-mail:qenome-reseascriken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsuura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashize
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa: Chordata;
Mammalia: Eutheria: Rodentia;
                                                                                                                                                                                                                                                                                                                                                     cleaved with XhoI and SstI. Cloning sites, 5' end: SstI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20530913
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                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MGD:MGT:1352464"
/db_xref="MGD:MGT:1902675"
                                                                                  /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                  Location/Qualifiers
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Sciurognathi; Muridae; Murinae; Mus
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Ratio: 1.841
Percent Similarity: 49.771
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                                                                                                                                                                                                                                                                                                           TGGATTATATTATGGATTCGTACAACAACAG.
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398 c 436 q
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151 leArgGluLeuMetAspAlaGlnMetLysThrPheAspThrThrPheSer 167
                                                                                                                                                                                                                                                                                                                                                                                         802 AACGGAA..........CTCACGGCAGACCAACAGACTCTCC 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 yThrGlnProLeuGlyValGlnGlyLeuThrGluGluGlnArqMetMetI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              652 GTATACAGGTTTGTTAACTGAAATCCAGTGTAAATCTAAACGGCTAAGGA 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 GAGTGCCGGCTAAGGAAGTGCAAAGAGATGGGGGATGTTGGCTGAATGTAT 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 ... AACGGGGGCAACTGCGTGATGGACATGTACATGCGCAGGAAGTGCCAG
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184 uProGluSerLeuGlnAlaProSerArgGluGluAlaAlaLysTrpSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             752 GGGCGTGACTTGCGACATGTGACCTCCACAACCAAGTTTTGCAGGGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 sGlyPhePheArqArqAlaMetLysArgAsnAlaArgLeuArgCysProP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 laAspGlu.....GluValGlyGlyProGlnIleCysArgValCysGly 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 AlaCysArqLeuArgLysCysLeuGluSerGlyMetLysLysGluMetIl 112
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                                                                                                                                                    HisPheLysAsnPheArgLeuProGlyValLeuSerSerGlyCysGluLe 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValGluGluArgArgAlaLeuIleLysArgLysLysSerGluArgThrGl 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAATGTGAAGCAGCACGCTGATCAGACAGCTAATGAGGACGACAGCGAA 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heArgLysGlyAlaCysGlulleThrArgLysThrArgArgGlnCysGln
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/clone_lib^"RIKEN_full-length_enriched_mouse_cDNA_library"
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq documentation block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: qb_est89:BF577692
                                                              TITLE
JOURNAL
                                                                                                                          AUTHORS
                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1354 CCCGCAGCAT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1304 CCCCTGCTTGAfGTGCTACAAAAGCTGTGCAAGATGTACCAGCCTGAGAA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1110 CAGACCTGTTGGAAGAAAGAATTCGAAAGAGT.....GGTATCTCTGAT 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1204 AATGACTCAGGAGGAGTACGCTCTGCTCAGAGGGATGGTCATCCTCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1060 GTTTCTTCGTTCGGCGGGAGATTTTCAATAAGAAACTTCCTGGCGGTCATG 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1010 GATCACGAAGATCAGATTGCTTTGCTCAAAGGGTCCGCAGTGGAGGCCAT 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1154 GAGTATATAACCCCGATGTTCAGTTTCTATAAAAGTGTTGGAGAACTCAA
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                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                 Mammalia: Entheria: Rodentia: Selurognathi: 1 (bases 1 to 689)
NIB-MGC http://mgc.ncl.nih.gov/.
                                                                                                                                                                                                                                           Mus musculus
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Email: cqapbs remail.nih.qov
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/lab_host="DH10B (TI phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                         US-09-276-935B-14 x AW158294
                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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JOURNAL
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                                                                                                                                             158 CGATGGGGACCCCAAGATCTGCCGTGCGTGTGGGGGACCGGGCCACTGGGT 207
                                                                                                                                                                                                                                   108 GAGGAGGAAGAAGACGCCTCTAACAGTTGTGGGAACGGGGGAAGACGAGGA 157
                                               208 ATCACTICAATGCTATGACCTGCGAGGGCTGCAAGGGATTCTTCAGGCGG 25:
                                                                                             51
                                                                                                                                                                  18 GluAspThrGluSerValProGlyLysProSerValAsnAlaAspGluGl 34
AlaMetLysArgAsnAlaArgLeuArgCysProPheArgLysGlyAlaCy 84
                                                                                             yrHisPheAsnValMetThrCysGluGlyCysLysGlyPhePheArgArg 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5', mRNA sequence.
AW158294
AW158294.1 GI:6270323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed sequence tags from Xenopus Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schutz.K., de la Bastide, M., Huang, E.N., Nascimento, L., Shah, R., Swaby, I., Shekher, M., Spiegel, L., Vil, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mccombie@cshl.orq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: Lambda Zap I; Site_1: Xbal; This library
was supplied by Holly Cline (Cold Spring Harbor Labs).
cDNA synthesis with oligo df Xba I (Xba I cloning Site).
RNA: stage 50-56 tadpoles, total brain tissue, GTC
extraction method." 80 *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="tadpole"
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/cell_line="W22-TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                           88.991
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4.015
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/clone_lib="Xenopus EST library"
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/db_xref="taxon:8355"
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KEYWORDS
SOURCE
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LOCUS AV652474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 AATGTCTGGACATCGGCATGAGGAAAGAGTTGATCATGTCCGATGCAGCG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ysCysLeuGluSerGlyMetLysLysGluMetIleMetSerAspGluAla 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 CGTCATCAACAAGAGCAATCGGCGCCACTGCCAGGCCTUTCGGCTCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
18 GluAspThrGluSerValProGlyLysProSer..........ValAs
                                                             30 GAGAAGCACGAGTCTGTGACAGCCACCCCAACACGTGACGTCATGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sGluIleThrArqLysThrArgArqGlnCysGlnAlaCysArqLeuArqL
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Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV652474 637 bp mRNA EST OF STATE 2000 AV652474 GLC Homo sapiens cDNA clone GLCDAG03 3', mRNA sequence.
                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 201203, P. R. China Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Zeguang Han
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: hanzq@chqc.sh.cn
This clone is available at CHGC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 637)
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xho!"
                                                                                                                                                                                                                                            387.50
2.533
56.044
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/tissue_type="corresponding non cancerous liver rissue"
/dev_stage="Adult"
/lab_host="SOLR"
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Percent Identity: 34.066
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seq name: qb_est76:BE573696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 SerAspCluAlaValGluGhuArqArqAlaLeutleLysArqLysLysSe 130
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Mos musculus
                                                  F.S.T.
                                                                          BE573696.1 G1:9817416
                                                                                                     BE57 (696
                                                                                                                     mkNA sequence.
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                                                                                                                                                                       1053 bp
                                                                                                                                                                             mRNA
                                                                                                                                                  Mus musculus cDNA clone IMAGE: 3710866 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213
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                                                                                                                                                                       15 AUG-2000
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alignment_block;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 09-276-935H-14 x HE573696
137 roleuGlyValGlnGlyLeuThrGluGluGlnArqMetMetIleArqGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 CUCTATGACCTGTGAAGGCTGCAAGGGTTTCTTCAGGCGGAGCATGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 COTOGGATOTOTOCACTIGTIGGAGACCGAGGGCCACGGGCTTCCACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 GCAAGGCCTGTTCACCTGCCCCTTC...AATGGAGATTGCCGCATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 raAshAlaArqLeuArqCysProPheArqLysGlyAlaCysGlulleThi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 nValMetThrCysGluGlyCysLysGlyPhePheArqArqAlaMetLysA 71
                                                                                                                                                                                                                                                                                                                                                  ArqLysThrArqArqGlnCysGlnAlaCysArqLeuArqLysCysLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProGln14eCysArqVa1CysGlyAspLysAlaThrGlyTyrHisPheAs
                                                                 TAAGCGAGATGATGATGAAGAAGGAAGGAAGAAGAGGCCTTGAAGGACA 443
                                                                                                                                                                                              uArqArqAlaLeulleLysArqLysLysSerGluArqThrGlyThrGlnP 147
                                                                                                                                                                                                                                                      userGlyMetLysLys.GluMetIleMetSerAsp.GluAlaValGluGl 120
                                                                                                                                                                                                                                                                                                                           AAGGACAACGGGGGACACTGCCAGGCCTGCCGGGTCAAACGCTGCGTGGA
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NHH-MCC http://mgc.nci.nih.qov/.
National Institutes of Health, Mammalian Gene Collection (MSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence start: 2
High quality sequence stop: 685.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: egaphs-ramail.mih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_bost "DH10H"
/note-"organ: mammary; Vector: pCMV SPORTS; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: oligo dT.
Library constructed by Lile Tochnologies. Investigator
providing samples: Jettrey Green, M.D., NIH"
a 362 c 274 q 173 t
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/sex "temale, virgin"
/lsssue_type="infiltrating dnetal carcinoma"
/lsssue_type="5 months"
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64.855
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/db_xref-"taxon:10090"
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AUTHORS
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VERSION
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LOCUS AW107536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444 GTCTGAGGCCCAAG...CTGTCTGAGGAGCAACAGCACATCATCGCCATC 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sValIleSerTyrPheArgAspLeuProIleGluAspGlnIleSerLeuL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuMetAspAlaGlnMetLysThrPheAspThrThrPheSerHisPheLy 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euLysGlyAlaAlaPheGluLeuCysGlnLeuArgPheAsnThr.ValPh 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AM107536 601 bp mRNA EST 20-OCT-1999 AU101405.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2159410 5' similar to qb.:03258 VITAMIN D3 RECEPTOR (HUMAN qb:U15548 Mus musculus beta 2 thyroid hormone receptor (MOUSE);,
                                                                                                               Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                               Unpublished (1999)
Other_ESTs: u191a06.x1
                                                                                                                                                                                                                                                                                                     Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person, B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW107536
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                                                            Fax: 314 286 1810
                                                                                                                                                                                                                                                                              The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 601)
l: mouseest@watson.wustl.edu
clone is available royalty-free through LLNL
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contact the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 CCTCGGATCTGTGGAGTGTGGAGACCGAGCCACGGGCTTCCACTTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 nValMetThrCysGluGlyCysLysGlyPhePheArgArgAlaMetLysA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 ProGlnIleCysArqValCysGlyAspLysAlaThrGlyTyrHisPheAs 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCTATGACCIGIGAAGGCTGCAAGGGTTTCTTCAGGCGGAGCAIGAAGC
                                                   uMetAspAlaGlnMetLysThrPheAspThrThrPheSerHisPheLysA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGACAACGGCGACACTGCCAGGCCTGCCGGCTCAAACGCTGCGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAAGGCCCTGTT CACCTGCCCCTT....AATGGAGATTGCCGCATCACC
GCTCGATGCCCACCACACACCTACGACCCCACCTATGCCGACTTCCGGG
                                                                                                               CTGAGGCCCAAG...CTGTCTGAGGAGCAACAGCACATTATCGCCATCCT
                                                                                                                                                                  LeuGlyValGlnGlyLeuThrGluGluGlnArgMetMetHeArqGluLe 154
                                                                                                                                                                                                                               AGCGAGAGATGATCATGAAGAGGAAGGAGGAAGAGGCCTTGAAGGACAGT 48
                                                                                                                                                                                                                                                                                     rgArgAlaLeuileLysArgLysLysSerGluArgThrGlyThrGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgLysThrArgArgGlnCysGlnAlaCysArgLeuArgLysCysLeuGl 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ingated to a praili adaptor [TGTTGGCCTACTGG], digested and cloned into distinct Draili sites of the pME18s-FL3 vector [5' site GACTGTGG, 3' site CACCATGTG). Xhol show be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGGCTAAAAAGCTGGG and 3' engage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer CGACCTGCAGCTCGAGCACA."
175 c 173 g 119 t
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was primed with an oligo(dT) primer
[AIGTGGCCTTTTTTTTTTTTTTTT]: double-stranded cDNA was
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/lab_host="DH10B"
/note="Ordan: kidney: Vector: pME18S-FL3; Site_1: LidIII
/note="Ordan: kidney: Vector: pME18S-FL3; Site_1: LidIII
/cacTGTGTG): Site_2: DraIII (CACCAIGTG): Ist strand cDNA
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/clone_lib="Sugano mouse kidney mkia"
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3.292
81.884
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Percent Identity: 51.449
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                                                                                                                                                                                                                     Align seg 1/1 to reverse of: A1768052
                                                                                                                                                                                                                                                                            US-09-276-935H-14 x A1768052/rev
                                                                                                                                                                                                                                                                                                                                                             Ratio: 2.980
Percent Similarity: 71.264
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     478
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                                                                                                             514 GTGTCTGTGAGAGCCTCACAGAAGAGCACCCCTGGGGGC
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                                                   15 THISCYSCHUASPThrGluSerValProGlyLysProSerValAsnAlu. 31
                                                                                                                                                           I LouGluValArqPro.....LysGluSerTrpAsuHisAlaAspPheVa 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTRICORGOTTOTA 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cONA Library Preparation: M. Bento Soares, Ph.D. cSNA Library Arrayed by: Great Lennor, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NNI-COAP clone distribution information can be tound through the L.M.A.G.E. Consortium/LLNL at: www bio.llnl.gov/bbr/plimage/limage.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg Ph.D.
Email: cdapbs:r≎mail.uihfqov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
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NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
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TROMOTANOCIGOCOOFIGO POOFICAGGAAGGAAGGCAATGGCGC-4-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inote "organ: colon: Vector: pTTT0-Pac (Pharmacia) with a modified polylinker; Site_1: Bot 1: Site_2: Boo RI: plasmid Juna from the normalized library NC1_CGAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified clunas from a pool of 5,000 clones made from the same library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subtraction by Reuto Soares and M. Fatima Bonaldo.
166 c = 160 g = 135 t = 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib "NCL_CGAP_Col6"
/tissue_type "colon tumor, RER+"
/lab_host-"DH10H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism #Homo sapiens"
/db_xret+"taxon:9606"
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                                                                                                                  SOHION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 CATGATGAAGGAGTTCATTCTGACAGATGAGGAAGTGCAGAGGAAGGGGG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 CACTATICACCITCCCCCTTC...AACGGGGACTGCCGCATCACCAAGGAC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 COAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 pAlaGimMettysThrPheAsp 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 ValGlnGlyLeuThrGluGlnGlnArgMetMetHeArgGluLeuMetAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 laLeulleLysArgLysLysSerGluArgThrGlyThrGlnProLeuGly 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 yMctLysLysGluMctIleMctSerAspGluAlaValGluGluArqArqA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 GACCTGTGAAGGCTGCAAAGGCTTCTTCAGGCGAAGCATGAAGCGGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 [hrArqArqdInCysdInAlaCysArqLouArqLysCysLoudInSertII 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 tfhrCysGluGlyCysLysGlyPhePheArqArqAlaMetLysArqAsnA 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 CGCCCGCCATAAGACCTATAAC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 CCCAAG...CTGTCTGAGGAGCAGCAGCAGCATCATTGCCATACTGCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACCGACGCCACTGCCAGGCCTGCCGGCTCAAACGCTGTGTGGACATCGG
                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Lite Technologies, Inc. cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BF102347
BF102347.1 GI:10884873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601751958F1 NC1_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3979358
                                                                                                                                                                    High quality sequence stop: 654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 654)
NIH-MGC http://mqc.nci.nih.qov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.S.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF102347
                                                                                                                                                                                                                        http://image.llnl.gov
                                                                                                                                                                                                                                                      tound through the L.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                          Email: eqapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia: Butheria:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa: Chordata: Cianiata: Vertebrata: Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....AspGludluValdlydlyProdin 49
                                                                                                                                                                                                 LLAM9173 row: d column: 15
/db_xref "taxon:10090"
/clone="IMAGE:3979358"
                                                       /strain "FVB/N"
                                                                                    ∕ordanism "Mus musculus"
                                                                                                                                         Location/Qualitiers
                                                                                                                     . 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rodentia; Sciuroquathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIKNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murinae:
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/tissue_type "tumor, biops

biopsy sample"

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alignment_block:
US-09-276-935B-14 x BF102347
                                                                                                                                                                                                                                                                                     seq_name: gb_est91:BF686868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
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                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: BF102347 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 snAlaArgLeuArgCysProPheArgLysGlyAlaCysGluIleThr.Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnIleCysArgValCysGlyAspLysAlaThrGlyTyrHisPheAsnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              etAspAlaGlnMetLysThrPheAspThrThrPheSerHisPheLysAsn 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGCATGATGAAGGAGTTCATCCTCACAGATGAGGAGGTGCAGCGTAAG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erGlyMetLysLysGluMetIleMetSerAspGluAlaValGluGluArg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACAACCGGCGACACTGCCAGGCCTGCCGGCTCAAACGCTGCGTGGACA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGCCCTGTTCACCTGCCCCTTC...AATGGAGATTGCCGCATCACCAAG
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                                                                                                                                                                                                                                                                                                                                             GCCACATCAG 613
                                                                                                                                                                                                                                                                                                                                                                                          uSerLeuGln 189
                                                                                                                                                                                                                                                                                                                                                                                                                                         INTCCGCCTCCAATTCGTGCAGACGTAAGTACCGGAAGCTATTCTCCAAG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheArgLeuPro.....GlyValLeuSerSerGlyCysGluLeuProGl 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGATGCCCACCACAAGACCTACGNACCCACCTATGCCGACTTCCGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGCCCAAG...CTGTCTGAGGAGCAACAGCACATTATCGCCATCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uGlyValGlnGlyLeuThrGluGluGlnArgMetMetIleArgGluLeuM 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAGAGATGATCATGAAGAGGAAGGAGGAGAAGAGGCCTTGAAGGACAGTCT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgAlaLeulleLysArgLysLysSerGluArgThrGlyThrGlnProLe 138
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                               Mus musculus
                                                                                                                        BF686868.1 GI:11972276
                                                                                                                                                 BF686868
                                                                                                                                                                     5', mRNA sequence
                                                                                                                                                                                              602102822F1 NCI_CGAP_Kid14 Mus
                                                                                                                                                                                                                       BF686868
                                                                           house mouse
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a 192 c 182 q 131 t 2 others
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3.127
76.623
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/lab_host="DH10B"
                                                                                                                                                                                                                    776 bp
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Percent Identity: 48.701
                                                                                                                                                                                                                         BRNA
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                                                                                                                                                                                                musculus
                                                                                                                                                                                                cDNA clone
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                                                                                                                                                                                                                    22-DEC-2000
                                                                                                                                                                                              IMAGE: 4221077
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alignment_block:
US-09-276-935B-14 x BF686868
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                               154 uMetAspAlaGlnMetLysThrPheAspThrThrPheSerHisPheLysA 171
                                                                                                          460
                                                                                                                                                                                                                   410
                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                                                                                                                                                                                                                                                                                                                                                                      310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 CCTCGCATCTGTGGAGTGTGTGGAGACCGAGCCACGGGCTTCCACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 rgAsnAlaArgLeuArgCysProPheArgLysGlyAlaCysGlulleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 nValMctThrCysGluGlyCysLysGlyPhePheArgArqAlaMctLysA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 ProGlnIleCysArqValCysGlyAspLysAlaThrGlyTyrHisPheAs 54
                                                                                                                                                                                                                   AGCGAGAGATGATCATGAAGAGGAAGGAGGGAAGAGGCCTTGAAGGACACI 459
                                                                                                                                                                                                                                                                                                                             CATTGGCATGATGAAGGAGTTCATCCTCACAGATGAGGAGGTGCAGCGTA
                                                                                                                                                                                                                                                                                                                                                          uSerGlyMotLysGluMetIleMetSerAspGluAlaValGluGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCGATGCCCACCACAAGACCTACGACCC.ACCTATGCCGACTTCCGGG
                                                                                                                                                             LeuGlyValGlnGlyLeuThrGluGluGlnArgMetMetIleArqGluLe 154
                                                                                                                                                                                                                                                                     rqArqAlaLeuIleLysArqLysLysSerGluArqThrGlyThrGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGACAACCGGCGACACTGCCAGGCCTGCCGGCTCAAACGCTGCGTGGA
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MCY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The L.M.A.G.F. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 663.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:4221077"
/clone_tib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pcMv-SPORT6: Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |*
a 231 c 215 g 160 t
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2.497
68.224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to:
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Percent Identity: 41.589
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732	229	682	6.17	6.45	202	606	981	556	1.7.1
732 CIPCIGITANCECIGGACTOTTP-COOTCICANIGCIGCGCCCAC 773	229 AlaAspSerGlyGlyLysGluTlePheSerLendeuProHis 242	682 (CMGCCAGCTTTTTCCACGACTGGGTCTGATGAAGAAGGGCTGCGATGACGT 73	219 sp61ySerValTrpAsnTyrLysPropro 22	6.45 GCCTCAAACTCTGAATCTGTAAGACCCCCCGCATTGAACACATGATGGAAC 6.8	202 lArdbysAsplacucysSerlacutysValSerlacuthntonArdtlythuA 21	6.0 Parameter Programme Pr	186 GluSerLeuGluAlaProSerArgGluGluAlaAlaLysTrpSerGlnVa 20	556 ACTTCCCGCCTCCAATTCGTCGCAGAGCTAAGTACAGGAGCGAGC	17) sulheArdieuProGlyVallæuSerSerGlyCysGlutæuPro 18
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Cenn2_6/ptcodata/lina/Sh_COMB_seq:US-08_643-61991 477.50 957.78 9.6e-46 2030 (cgn2_6/ptcodata/lina/Sh_COMB_seq:US-08_130-2831 477.50 957.78 9.6e-46 2030 (cgn2_6/ptcodata/lina/Sh_COMB_seq:US-08_130-2831 477.50 957.78 9.6e-46 2030 (cgn2_6/ptcodata/lina/Sh_COMB_seq:US-08_130-2831 477.50 957.78 9.6e-46 2030 (cgn2_6/ptcodata/lina/pcTUS_COMB_seq:US-08_130-2831 477.50 930.61 31e-44 1860 (cgn2_6/ptcodata/lina/pcTUS_COMB_seq:US-08_130-2831 477.00 930.61 31e-44 1860 (cgn2_6/ptcodata/lina/pcTUS_COMB_seq:US-08_130-2931 477.00 930.61 31e-43 1659 (cgn2_6/ptcodata/lina/pcTUS_COMB_seq:US-08_130-2931 477.00 930.61 31e-43 1677 (cgn2_6/ptcodata/lina/pcTUS_COMB_seq:US-08_130-2931 477.00 930.61 31e-43 1677 (cgn2_6/ptcodata/lina/pcTUS_COMB_seq:US-08_130-393 300.61 31e-43 1677 (cgn2_6/ptcodata/lina/pcTUS_COMB_seq:US-08_105-130-393 300.61 31e-43 1677 (cgn2_6/ptcodata/lina/pcT
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Database sequences: 317530
Database length: 92630169
Search time (sec): 93.020000
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Query: US-09-276-935B-14
Query length: 414
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-Q-/cqr2_L/USPTO_spool/USO9276935/runat_11072001_091608_14560/app_query.fasta_1.480
-Q-/cqr2_L/USPTO_spool/USO9276935/runat_11072001_091608_14560/app_query.fasta_1.480
-Q-/cqr2_L/USPTO_spool/USO9276935-sUFFIX=p2n.rui
-GAPOP=12.000 -Q-/cqr2_1000 -MINMATCH-0.100 -LOPGL=0.000
-LOOPEXT=0.000 -Q-/cqr2_1000 -Q-/cqr2_10.000
-XGAPEXT=0.000 -Q-/cqr2_10.000 -Y-/cqr2_10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FCAPEXT=7.000 -Y-/cqr2_10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=DLOSUMG2 -TRANS=-human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFNT=pfs -NORM-ext -MINLEN=0 -MAXLEN=200000000
-USER-USO9276935_@CGN1_1_62 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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US-09-276-531-111
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ATTORNEY/AGENT IN
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/cgn2_6/ptodata/l/ina/PCTUS_COMB.seq:PCT-US92-02:20A-1 + 372.00 731.47 + 87cg02_6/ptodata/l/ina/Sa_COMB.seq:US-08-892-47-13 + 372.00 729.83 4.86-3 / cgn2_6/ptodata/l/ina/Sa_COMB.seq:US-08-592-383-1 469.00 729.80 8.08 + 200-329.80 8.08 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.09 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.80 8.00 - 200-329.8
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                                                                                              US-09-276-935B-14 x US-09-276-531-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 31...
STREET: 31...
STREET: ALTO
CITY: PALO ALTO
STATE: CALIFORNIA
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reddy, Roopa
APPLICANT: Guedler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PR. NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 801 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: LYON E. MUTTY, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  Quality: 1044.00
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Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SINTFET 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INCYTE PHARMACEUTICALS, INC
US-09-276-531-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     March 27, 1998
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from: 1
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to:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/07737736H
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                               APPLICANT: Deluca, Hector
APPLICANT: Ross, Troy K.
APPLICANT: Prahl, Jean M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 lyThrGlnProLeuGlyValGlnGlyLeuThrGluGluGlnArqMetMet 150
                                                                                                                                                                                                          TITLE OF INVENTION: Method of Producting
TITLE OF INVENTION: 1,25-bibydroxyvitamin by Receptor Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 r. ilis . PholysAsnPhoArgLouProClyValLouSerSerGlyCysGl 184 [ 111 [ 111 [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 11] [ 12] [ 13]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             547 GGACITCAGCCACTGGGAGTGCAGGGGGCTGACAGAGGAGCAGCGGATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447
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                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        796 GGGG 799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        597 AFCAGGAGCTGATGGACGCTCAGATGAAAACCTTTGGACACTACCTTCTC 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497 COTGGAGGAGAGGCGGCCTTGATCAAGCGGAAGAAAGTGAACGGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 TGAGGACAGAGTGTGTTGCTTGGAAAGCCAGTGTCAACGCAGATGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 s6huAspTht6huSerValPro6lyLysProSerValAsnAlaAsp6hu6 34
                                                                                         ADDRESSEE: Carl R. Schwartz, cont. STREET: 411 East Wisconsin Avenue
                   COUNTRY:
                                                                           CITY: Milwaukee
                                                     STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCCGGTGCCGGAAGATCTGTGGTGTTTGAAGTCT, TOTCTTGCAGCTGG 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aValtilutluArqArqAlaLeulleLysArqLysLysSertiluArgThrG=134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerGluValArqLysAspLeuCysSerteutLysValSerteutGluLeuAr 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GETTGCAGAGTCTCTGCANGCCCCATCGAGGGGAAGAAGCTGCCAAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrHisPheAsnValMeTThrCysGluGlyCysLysGlyPhePheArqAr 67
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20285
                                          Wisconsin
                                                                                                                                                                                                                                                                                                                        Defines, Hector F.
                      1 S. A
                                                                                                                           . Schwartz, Esq., c/o Quarles
                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seq 1/1 to: US-07-737-736B-6 from: 1 to: 2043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-276-935B-14 x US 07-737-736B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [NFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLEAGE: NO MOLEAGE: NO
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CURKENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2043 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTERNEY/AGENT INFORMATION:
               121 rgArgAlaLeulleLysArgLysLysSerGluArgThrGlyThrGlnPro 137
                                                               352 CATCGGCATGATGAAGGAGTTCATCCTGACAGATGAGGAGGAGGTACAGCGTA 401
                                                                                                                                                                                                                                  255 GGAAGGGGCTGTTCACCTGTCCCTTC...AATGGAGATTGCCGCATCACC 30
                                                                                                                                                                                                                                                                                                                                                                                                       155 CCCCGGATCTGTGGAGTGTGTGGAGACGGAGGCCACAGGCTTCCACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                     54 nValMetThrCysGluGlyCysLysGlyPhePheArqArqAlaMetLysA 71
                                                                                                                                                                                                                                                                          71 rqAsnAiaArqLeuArqCysProPheArqLysGlyAlaCysGlnHeThr
                                                                                                                                                                                                                                                                                                                                                                                                                           38 ProGlulleCysArqValCysGlyAspLysAlaThrGlyTyrHisPhcAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTHORS: Wiese, Russell J.
ANTHORS: Maeda, No. 5260199uyo
ANTHORS: Deluca, hector F.
TITLE: Structure and regulation of the rat
TITLE: 1,25-dihydroxyvitamin D3 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: NUCLEIC ACID STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAGES: 9499-9502
DATE: December-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : ASOTOHOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 414-277-5774
                                                                                                     userGlyMetLysLysGluMetlleMetSerAspGluAlaValGluGluA
                                                                                                                                                   AAGGACAACCGGCGACACTGCCAGGCCTGCCGGCTCAAACGCTGTGGGA
                                                                                                                                                                                      ArglysThrArgArgGlnCysGlnAlaCysArgLeuArgLysCysLeuGl 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /AGENT in. .
Schwartz, Carl R.
Schwartz, Carl R.
Schwartz, Carl R.
Schwartz, Carl R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
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2.712
68.537
US/07/737,736B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96-296-2185-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                 351
                                                                                                                                                                                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                                                      254
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1321	ACTCCAAACAATACCGCTCCCTCTCCTTCCAGCCCGAGAATAGCATGAAG	272
400		400
400 1271	eLeuLysileMetAlaMetLeuThrGluPhe : :::::::::::::::::::::::::	390 222
390 1221	LysSerTyrileGluCysAsnArgProGlnProAlaHisArgPheLeuPh ::::: :::	37 4 172
373 1171	euGlnHisArgValValAspGlnLeuGTnGluGlnPheAlaIleThrLeu ::: :::::::::	357 122
357 1121	rValLeuMetGlnAlaTleSerLeuPheSerProAspArgProGlyValL: :::::	340 072
340 1071	YrMetLeuLysLysLeuGlnLeuH TGCGGCTGAAGAAGCTGAACTTAC	32 4 022
323 1021	AlaGlyGlyPheGlnGl ::: AAAGCTGGGCACACCCT	310 972
310 971	ThrGlyThrTrpGluCysGlyArgLeuSerTyrCysL 	293 922
293 921	ValPheAs :: TCTTTCAC	277 872
276 871	allleSerTyrPhcArgAspLeuProlleGluAspGlnIleSerLeuLeu ::	260 822
260 821	tAlaAspMetSerThrTyrMetPheLysClyileIleSerPheAlaLysV: ::::::::::::::::::::::::::::	243 772
243 771	ysGlullePheSerLeuLeuProHisMe ::: ::: ::: :: TGTCTCCTCTCCATGCTGCCCACCT	227 722
226 721	SerLeuGlnLeuArgGlyGluAspGlySerValTrpAsnTyrLys ::: ::: :::	212 587
211 686	ysAspleucysSerLeuLysVal	202 537
202 636	LeuGinAlaProSerArgGluGluAlaAlaLySTrpSerGlnVa ::::::::::::::: :::::::::: :::::	186 599
185 598	SnPheArqLeuProGlyValLeuSerSerGlyCysGluLeuPro ::	171 549
171 548	uMetAspAlaGlnMetLysThrPheAspThrThrPheSerHisPheLysA 	199
154 498	LeuGlyValGlnGlyLeuThrGluGluGlnArgMetMetfleArgGluLe	152
	VIGATAATGAAGAGAAAAGAGGAAGAG	, 12

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; PAGES: 3294-3298
; DATE: May-1988
US-07-737-7368-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptcdata/1/ina/5A_COMB.seq:US-07-737-736B-5
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Deluca, Hector F.
APPLICANT: Ross, Troy K.
APPLICANT: Ross, Troy K.
APPLICANT: Prahl, Jean M.
TITLE OF INVENTION: Method of Producing
TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/737
ETLING DATE: 19910730
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Carl R.
REGISTRATION NUMBER: 29,437
REFERENCE/DOCKET NUMBER: 96-27
TELEOPHONE: 414-277-5715
TELEPHONE: 414-277-5717
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1322 CTCACACCCCTTGTGCTGGAGGTGTTCGGC 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
AUTHORS: Baker, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1399 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 AlaThrProLeuMetGlnGluLeuPheGly 410
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Carl R. STREET: 411 Fast W CITY: Milwaukee STATE: Wisconsin
                                                                                                                                                                                                                                                                                      AUTHORS:
AUTHORS:
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-005
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                        TITLE: Cloning and expression of full-length cDNA TITLE: encoding human vitamin D receptor JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                       AUTHORS: AUTHORS:
                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 53202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                    VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Application US/07737736B 5260199
                                                                                                                         85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Carl R. Schwartz, Esq., c/o Quarles & Brady
411 East Wisconsin Avenue
                                                                                                                                                                                                                                            Hughes, Mark
Crisp, Tracey M.
Mangelsdorf, David J.
Haussler, Mark R.
Pike, J. W.
                                                                                                                                                                                                          O'Malley, Bert W.
                                                                                                                                                                                                                                                                                                                                                                         Baker, Andrew R
                                                                                                                                                                                                                             Shine, John
                                                                                                                                                                                                                                                                                                                                                    McDonnell, Donald P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/07/737,736B
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Quality:

Hality: 750.00 Ratio: 2.688

Length: Gaps:

allignment block: Align seq 1/1 to: US-07-737 736B-5 trom: 1 to: 1399 US-09-276-935B-14-x-US-07-737-736B-5 Percent Similarity: 67.718 Percent Identity: 40.291 849 CTAACATGATACCAGGATTCAGAGACCTCAGCTCTGAGGACCAGATCGTA 258 laLysVallleSerTyrPheArgAspLeuProlleGluAspGlnIleSer 755 225 TyrLysProProAlaAspSerGlyGlyLysGlullePheSerLeuLeuPr 241 664 CTCCTCCTCGCTCAGATCACTGTATCACCTCTTTAGACATGATGGACTCGT 713 620 184 LeuProGluSerlæuGluAlaProSerArgGluGluAlaAlaLysTrpSe 200 520 GCTGGACGCCCACCATAAGACCTACGACCCCACCTACTCCGACTTCTGCC 569 473 CTGCGGCCAAG...CTGTCTGAGGAGCAGCAGCATCATTGCCATACT 138 LeuGlyValGluGlyLeuThrGluGluGlnArgMetMetHeArgGluLe 154 04 899 CEGNEGAAGTCAAGTGCCATTGAGGTCATCATGGCGTTGCAATGAGTC 948 199 CONCERGROPAGE TO GET CAGE TACAGE AT COMMAND GET A FING CETTER 24 | OHISMetAlaAspMetSerThrTyrMetPheLysGlyTleTteSerPheA 208 erheibysValSerbeuGlibeuArgGlyGluAspGlySerValTrpAsii 224 154 uMetAspAlaGlnMetLysThrPheAspThrThrPheSerHisPheLysA 171 4.23 AGCCGGAGATGATCCTGAAGCGGAAGGAAGGAGGAGGCCTTGAAGGACAGT 472 121 rqArqAlafoutlelysArqLysLysSerGluArqThrGlyThrGlnPro 137 373 CATEGUCATGATGAAGGAGTTCATTCTGACAGATGAGGAAGTGCAGAGAGGA 422 226 TOCTATOACCTGTGAAGGCTGCAAAGGCTTCTTCAGGCGAAGCATGAAGC 176 CCCCGGATCTGTGGGGGTGTGTGGAGACCGAGCCACTGGCTTTCACTTCAA 22° Ξ 88 Proffin HedysArdValdysClyAspLysAlaThrGlyTyrHisPheAs 54 LeuLeuLysClyAlaAlaPheGluLeuCysGluLeuArgPheAsnThrVa CCAGCTTCTCCAATCTGGATCTGAAGTGAAGAAGATTCAGAT..... AGGCCCAACTCCAGACACACTCCCAGC.....TTCTCTCTGGGGACTCCTC 663 ArgLysThrArqArqGlnCysGlnAlaCysArqLeuArqLysCysLeuGl 104

	TICS	
	: INFORMATION FOR SECTIONO: 1:	
	ELEFAX: (617) 542-8906	
	FORMATIC	
	REFERENCE/ISSIKET NUMBER: - 00786/126001	
	NAME: Paul T. Clark	
	ي د	
	APPLICATION NUMBER: 07/843, 350	
	PRIOR APPLICATION DATA:	
	CLASSIFICATION: 4.55	
	APPLICATION NUMBER: US/08/459,489	
	Ē	
	OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)	
	9 ·	
	STATE: Massachusetts	
	=	
	ADDRESSEE: Fish & Richardson	
	DENCE ADDRESS:	
	: NUMBER OF SEQUENCES: 10	
	CAR RECEPTORS	
	seq_documentation_piock: ; Sequence 1, Application US/08459489	
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	401AlaThrProLeuMetGlnCluLeuPheGly 410	
1 14	1299 AGGAGCACTCCAAGCAGTACCGCTGCCTCTCCTTCCAGCCTGAGTGCAGC	
400	400	
129	1249 GCTCTATGCCAAGATGATCCAGAAGCTAGCCGACCTGCGCAGCCTCAATG	
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£8	372 ThrLeuLysSerTyrlleGluCysAsnArgProGlnProAlaHisArgPh	
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114	1099 GGAGCATGTCCTGCTCATGGCCATCTGCATCGTCTCCCCAGATCGTCCTG	
355	338 uGluTyrValLeuMetGlmAlalleSerLeuPheSerProAspArqProd	
109	1049 CCCCTCATCAAGTTCCAGGTGGGACTGAAGAAGCTGAACTTGCATGAGGA	
38	322 ProMetLeubysPheHisTyrMetLeubysLysLeuGlabeuHisGluGl	
104	999 ACCOCOTCAGTGACCTGACCCAAAGCCGGACACAGCCTGGAGCTGATTGAG	
321	307CysteenGluAspThrAlaGlyGlyPheGlnGInLeuLeuGlu	
86.6	949 CTTCACCATGGACGACATCTCCTGGACCTGTGGCAACCCAAGACTACAAGT	

TYT	1450 ucleic acid	
TO: 1S-08-459	: linear	
lignment_	_scores: Quality: 744.50 Leng	
Percent :	rity: 61.224 Percent Identity: 38.32	
lignment. US-09-27	t_block: 76-935B-14 x US-08-459-489-1	
Aliyn se	g 1/1 to: US-08-459-489-1 fr	
153	ArgProLysGluSerTrpAsnHisAlaAspPh 1 :::	14 202
14 - 203 -	eValHisCysGluAspThrGluSerValProG 2	25 252
25 253 (lyLysProSerValAsnAlaAspGluGluValGlyGly : :	37 296
38 297	ProGlnileCysArgValCysGlyAspLysAlaThrGlyTyrHisPheAs 5:::	54 343
344	nValMetThrcysGludlyCysLysGlyPhePheArgArgAlaMetLysa :	71 393
71 394	rgAsnAlaArgLeuArgCysProPheArgLysGlyAlaCysGluileThr E ::::::: AAAGCATTGGTCCCACCTGCCCCTTTGCTGGAAGCTGTGAAGTCAGC	87 440
88 . 441	ArgLysThrArgArgGinCysGlnAlaCysArgLeuArgLysCysLeuGl :::	104 490
10 4 491	uSerGlyMetLysLysGluMetTleMetSerAspGluAlaValGluGluA::::	121 540
121 541	rgArgAlaLeulleLysArgLysLysSerGluArgThrGlyThrGlnPro:	137 587
138 588	LeuGlyValGlnGlyLeuThrGluGluGlnArqMetMetILeArqGluLe:	154 622
154 623	UMCTASPAlaGlnMetLysThrPheAspThrThrPheSerHisPheLysA	171 672
171 673	<pre>snPheArgLeuProGlyValLeuSerSerGlyCysGluLeuProGluSer ::: </pre>	187 719
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204	sAspLeuCysSerLeuLysValSerLeuClnLeuArgGlyGluAspGlyS	221
721		7

	OPERATING SYSTEM: IBM P.C.	
	MEDIUM TYPE: 3.5" Diskette, 1.44 Mb	
	COMPUTER READABLE F	
	COUNTRY: U.S.A.	
	STATE	
	STREET: 225 Franklin Stre	
	CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richards	
	NUMBER OF SEQUENCES: 10	
	TITLE OF INVENTION: MOLECULES	
	APPLICANT: David D. Moore et al.	
	Patent No. GENERAL 1	
	documentation_b	
	qn2_6/ptod	
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	403ProLeuMetGInGluLeu 408	
128	38 TAATGAGGCCTACGGGTACCAAATCC	
402		
123		
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108	TATGTGCTCTTGGCTGCCATGGCCCTGTTCTCTCCTG	
353	luGluGluTyrValLeuMetGlnAlaIleSerLeuPheSerProAspA	
103	AGTTGCTCTTTCACTTCCATGGAACACTACGAAAACTGCAGCTCC	
ũ	20 euGluProMetLeuLysPheHisTyrMetLeuLysLysLeuGluLeuHi	
186	CUCTACACATTUAAGATUGAGUCUGTGTGGGGTTCCAUGTAGAGT FI	
N	04 uScrTyrCysLeuGluAspThrAlaGlyGlyPheGlnGlnLeuI	
437	88 CTCAATACCACITTCTGTCTCCAAACACAAAACTTCCTCTGCGGGCCTC	
304	eAsnThrValPheAsnAlaGluThrGlyThrTr	
8 H 7	CCAGATCTCCCTTCTCAAGGGAGCAGCTGTGGAAATCTGTCACAT	
287	InfleSert.cut.cut.ysGlyAlaAlaPheGlut.cuCysGlnf	
837	ATCAAGTTTACTAAGGACCTGCCCGTCTTCCGTTCCCTGCCCATTGAA	
271	.eAlaLysValIleSerTyrPheArgAs ::: ::: ::	
787	CTTCGCAGACATCAACACTT	
254	euLeuPrcHisMetAlaAspMetSerThrTyrMetPheLysGlyL	
737	732	
237	. =	

SOFTWARE: WordPortect (Version 5.0) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/ASB,686 FILING DATE: CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 07/843, 350
FILING DATE: February 26, 1992 AFTORNEY/AGENT INFORMATION: NAME: FIGURE CLIFE
RECIEVATION NUMBER: 40,162 REFERENCE/DACKET NUMBER: 00786/126001
TELEPOMMUNICATION INFORMATION: TELEPIONE: (617) 542 5070 TELEPAX: (617) 542-8906
TELEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1450 TYPE: nucleic acid STRANDEDNESS: single TOPOLYCY: linear \$ 08-458-686-1
lignment_scores: Quality: 744.50 Length: 441 Ratio: 2.757 Gaps: 11 Percent Similarity: 61.224 Percent Identity: 88.422
lignment_block: JS-09-276-9458-14-x-US-08-458-686-1
4 ArgProlysGluSerTrpAsnHisAlaAspPh 14 :::
14 PValH)stys
25 TytysProSerValAshAlaAspGhaGhaGhaGhaghgHgH7 97 ::
48 ProfibilecysatqValCysGlyAspLysalJThtGlyTytHisPheas 54 ::: [[] [[] [] [] [] [] [] [] [] [] [] [] [
'4 nvalmet Threysol uolycystysolyphepheargargariamettysa 71
71 rgAsnAlaArglænArgdysProPheArglysGlyAladysGlu11eThr 87 ::::: [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]
HH ArgLysThrargargGlocysGloalar'ysargLeolarglysCysLood] 104 ::: TITLIT:::
104 uSor GlyMet LystlysGluMet HeMet SerAspGluAldValchuGluA 121 - CCCCH) J.H.C.C.H.H.C.C.H.H.H.C.C.H.H.H.C.C.H.H.H.L.C.H. 491 TGCTGGCATGAGGAAAGACATGAYAATGTCGGCAGAAGCCCTGGCATTGC 540
121 rgArgAlaLwullefiysArgliysLysSergluArgThrGlyThrGlnPro 137 [111111] 541 GGCGAGCAAGCAGGCCCAGCGGGGGACAGAGAAAACACCTGTGCAA 587
138 TzeuGlyVa1GluGlyLeedThrGluGluGluArgMetMetTleArgGluLe 154

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5.47 10.47	euglufrometheubystheHistyrMet 	
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304 937	PhoAsnThrValPhoAsnAlaGluThrGlyThrTrpGluCysGlyA	288 888
287 887	Sp@lulleSerl@uLeuLys@lyAlaAlaPhe@luLeuCys@lnLeu 	271 838
271 837	#11eSerPheAldLysVall1eSerTyrPheArqAspLegPr 	254 788
25 4 787	SerLeuteuProHisMetAlaAspMetSerThrTyrMetPhet 	238 738
	oTocic	ا ند
741	orValTrpAsgTvrlvsproProAlaAsgSorGlvGlvlvsGlulleph	741 221
	AspleuCysSerLeuLysValSerLeuGlnLeuArqGlyGluAspGly	
7 (1	LeudinAlabroSerArgGinGluAlaAlaDysErpSerGinValArgLy - ACCCTGGCCCT	720
_	:: HHHH	7
x	PheArdteuProtteVallauserser() vcvs(tulauProtthser	171
171 672	uMet AspAl ad limet LysThrPheAspThrThr PheSerHiseheLysA 	154 623
622	CTGAGTAAdGAGAAGAAGAAGATCTGATCCGGACACT	

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TOPOLOGY: linear US-07-843-350C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 744.50
Ratio: 2.757
Percent Similarity: 61.224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-07-843-350C-1 from: 1 to: 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-276-935B-14 x US-07-843-350C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/POCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 542-5070
TELEPA: (617) 542-8906
TELEX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: David D. Moore et al.
TITLE OF INVENTION: CAR RECEPTORS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/843,: FILING DATE: February 26, 1992 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
                                                                                              297
                                                                                                                                                                                                                                                                                     203 TGTGGCCTGCAGGTGACATGCTGCCTAAGAGAAGCAGGAGTCTGTGACAG 252
                                                                                                                                                                                                                                                                                                                                                                              153 AAACCAGCAACAGCGTGGGAGTTTGGGGGAGAGGCATTCCATACCAGATTC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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344 TGCGCTGACTTGTGAGGGCTGCAAGGGTTTCTTCAGGAGAACAGTCAGCA 393
                 54 nValMetThrCysGluGlyCysLysGlyPhePheArgArgAlaMetLysA 71
                                                                                                                                                                                                                                                                                                              38 ProGlnIleCysArgValCysGlyAspLysAlaThrGlyTyrHisPheAs 54
                                                                                                                                                                                                                                 25 lyLysProSer......ValAsnAlaAspGluGluValGlyGly 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 225 I
                                                                                                                                                                                                                                                                                                                                                                                                                           4 ArgProLysGluSerTrp......AsnHisAla.....AspPh 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                         ...AGGAACTGTGTGGTATGTGGGGACCAAGCCACAGGCTACCACTTTAA 343
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Caps: 11
Percent Identity: 38.322
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0	CCTGAGTATGTGCTCTTGGC	الما
بين 55 يا	 luGluGluTvrValLeuMetGlnAlaIleSerLeuPheSerProAs	337
336 1037	euGluProMetLeuLysPheHisTyrMetLeuLysLysLeuGluLeuHis :::::: :::	320 988
987	:::	938
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404 937	alPheAsnAlaGluThrGlyThrTrpGluCys6lyArqLe :: :::	288 888
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271 837	TPheArgAspLeuProIleGluA ::: CTTCCGTTCCCTGCCCATTGAAG	25 4 788
œ	:::	تب
Jn	uProHisMetAlaAspMetSerThrTvrMetPheLysGlyIl	تب
7 5 7	:::::: CTGCTG	732
237	/alTrpAsnTyrLysProProAlaAspSerGlyGlyLysGluIlePhe	221
731		731
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187 719	<pre>snPhcArqLeuProGlyValLeuSerSerGlyCysGluLeuProGluSer :: </pre>	171 673
	::	Ñ
~J	MetAspAlaGlnMetLysThrPhcAspThrThrPheSerHisPheLysA	UT .
154 622	ValGlnGlyLeuThrGluGluGlnArqMetMetIleArqGluLe 	138 588
œ	AGCAGGCCCAGCGGGCACAGCAAACACCTGTGCAA	4-
.eu	qArqAlaLeuIleLvsArqLvsLvsSerGluArqThrGlvThrGlnPro	121
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	SEQUENCE CHARACTERISTICS:
	TELEPHONE: (617) 542-5070 TELEPAX: (617) 542-8906
	REGISTRATION NUMBER: 0,162 REFERENCEZOCKET NUMBER: 00786/126001
	ATTORNEY JASENT INFORMATION: NAME: Paul T. Clark
	PRIOR APPLICATION NUMBER: US/07/843, 850 PILLM: DAYE PERFOREY 26 1892
	FILING DATE: 19930222 CLASSIFICATION:
	CURRENT APPLICATION DATA:
	SOFWARE: WordPerfeet (Version 5.0)
	COMPUTER: 18M PS/2 Model 502 or 55X
	COMPUTER REALIZABLE FORM:
	줐
	STREET: 225 Franklin Street CTTY: Boston
	; CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson
	: TITLE OF INVENTION: METHODS : NUMBER OF SEQUENCES: 8
LES AND	APPLICANT: DAVID D. MOORE ET AL. TITLE OF INVENTION: CAR RECEPTORS AND RELATED MOLECULES
	seq documentation_block: Sequence L_Application_PC/TUS9301559 : GENERAL_INFORMATION
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	403ProLeuMetGlpGluLeu 408
A 1287	Techoene
. 402	4.02
. 402 F 1237	387 Argehetzenbhetzenbys Hewer AlamertzenbhrottobheAlathr
T 1187	

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287 887	pGLnTleSerLeuteutysGlyAlaAlaPheGluteutysGlnT 	
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254 787	LeuLeuProHisMetAlaAspMetSerThrTyrMetPhelysGly - - - -	
7.47	rValfrpAsuTyrLysProProA	221 742
- N	Aspiteut ys et Lamby s val set trade i internatique i you maspo	7 4 1
204 7.41	@InAlaProSerArqGluthuAlaAlatySTrpSorGlnValArqL 	: N 30:
187	uProdtyValLeuS 	171 673
171 672	Aet LysThrPh ::: ACCCGCCACAT	154 623
154	31 yValGlbGlyLeuT 	1 48 588
1.47	dA) aLeu HelysArqbysLysSerGluArqThrGlyPhrGlbt 	121 541
121 540	LysLysGluMetfloMetSerAspGluAldValdludl 	104 491
104	LysThrArqArqGlbC - - - -	88 441
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seq_documentation_block:
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; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1138 CACTGACTCTGCAAAGCTACATCAAGGGCCAGCGAGCGAAGGCCCCGGGAT 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1088 ACCTGGAGTTACCCAGAGAGATGAGATTGATCAGCTGCAAGAGGAGGATGG 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 ArgPheLeuPheLeuLysIleMetAlaMetLeuThrGluPheAlaThr.. 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 laIleThrLeuLysSerTyrIleGluCysAsnArgProGlnProAlaHis 386
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                                                                                                                                        REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD154P--
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BARBARA S. KITCHEL
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US94/12883 FILING DATE: Concurrently Herewith CLASSIFICATION:
                                                                                            TELEFAX:
                                                                                                                                                                                                                                                             FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. B
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                               TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                           TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uSerTyrCysLeuGluAspThrAiaGly...GlyPhcGlnGlnLeuLeuL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAATGAGGCCTACGGGTACCAAATCCAGCACATCCAGGGCCTGTCTGCCA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluGluTyrValLeuMetGlnAlaIleSerLcuPheSerFroAspAr 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGTTTCTGTATGCGAAGTTGCTAGGCCTGCTGGCTGAGCTCCGGAGCAT 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gProGlyValLeuGlnHisArgValValAspGlnLeuGlnGluGlnPheA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAGTTGCTCTTCACTTCCATGGAACACTACGAAAACTGCAGCTCCAA 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77210
                                                                           79-0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                               Concurrently Herewith
                                                                                                                                                                                                                                                                                        10-NOV-1993
                                                                                                                                                                                                                 KITCHELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UBIQUITOUS NUCLEAR RECEPTOR: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                              US 08/152,003
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (ger
PCT-US94-12883-3
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                                                                                                                                                                                                                                                                                                                                                                                            483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 ACGAGCTTTGCCGTGTCTGTGGGGACAAGGCCTCCGGCTTCCACTACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                       120 uArqArqAlaLeuIleLysArqLysLysSerGluArqThrGlyThrGln. 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 pThrGluSerVal.ProGly.....LysProScrValAsnAlaAspGlu 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 ProLysGluSerTrpAsnHisAlaAspPhcValHisCysGlu.....As
                                                                                                                                                                                                                                                                                           CGCAGTCACCTGTGGGGCCGCAGGGCAGCAGCAGCTCAGCCTCTGGGCCT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGCAGGGATGAGGGAGCAGTGCGTCCTTTCTGAAGAACAGATCCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qAsnAlaArqLeuArqCysProPheArq...LysGlyAlaCysGluIleT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCTCAGCTGCGAAGGCTGCAAGGGCTTCTTCCGGCGCAGTGTGGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValMetThrCysGluGlyCysLysGlyPhePheArgArgAlaMetLysAr 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAACCAGAGCGCAAGAGAAAGAAGGGGCCCAGCCCCGAAGATGCTGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGCCAGCTCAGCCTGCAGCAGACTGGGTCATCCCAGATCCCGAAGA 182
TGGCGGCCCAACTGCAGTGCAACAAACGCTCCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCCTTTCATGCGGCGCAAGTGCCAGCAGTGCCGGCTGCGCAAGTGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hrArgLysThrArgArqGlnCysGlnAlaCysArqLeuArqLysCysLeu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roGlnIleCysArgValCysGlyAspLysAlaThrGlyTyrHisPheAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGTGGGGCCAGGCGCTATGCCTGCCGGGGTGGCGGAACCTGCCAGATGG
                                                                                                AGAGGGTGTCCAGCTAACAGCGGCTCAAGAACTAATGATCCAGCAGTTGG
                                                                                                                                        ....LeuThrGluGluGlnArgMetMetlleArgGluLeuM 155
                                                                                                                                                                                                                                                                                                                                         .....ProLeuGlyValGlnGly.......
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1.844
52.113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
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26.761
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	APPLICANT: NAKAMUKA, YUSUKE APPLICANT: SALTO, HIROKO TITLE OF INVENTION: BUDN PROTEIN AND DNA
	eq documentat Sequence 1, Patent No. (
_	seq.name: /eqn2_6/ptodata/1/ina/58_COMB.seq:US_08_649_6198
	402ThrProfauMetGluGbulauPheGlylle 411 [[H]] EEEEEGURECGAAAFETGGGAACETE 1-859
401 1320	98 hr 14 21 egerga
1270	- 4 D =
1220	67 GludinéhoAlaileThriconlysSerTyriledlucysAsnArgProdi ::: ::::: ::: :: :::
366 1170	60 etProAspArqProGlyValLeudInBisArqValValAspGInLeudIn T. H.H.H.H.H.F.; E.H. E.; H.H.F.; H.H.H.H.H.H.F.; H.H.H.H.H.H.H.H.H.H.H.H.H.H.H.H.H.H.H
450 1120	OF THE CONTRACT OF THE CONTRAC
1070	417 GlidandandiluProMetLonLysPhoHisfyrMetLonLysLyslo 3- 1021 GIGGNGTTCATCAACCCCATCTTCGAGTTCTCGCGGGGCCATGCGCGCCCT 1
916	402 GlyAraLouSerTyrCysLoudluAsp Thi Aladlydlythodlin
401 970	288 eAsnitaValPheAsnAladhuthrdlythrtipdheys 930 AGCGMGGCGCIACAACCAGGAGA
288 929	272 GlulleSerfauleutysGlyAlaAlaPhedluteuCysGluteuArqPh
271 879	255 TeSer PhoAlaLysValTTeSerTyrPhoArqAspLouProfTeGTuAsp
255 829	· -
788	. 4
	No.
221	l'enc.
205 741	
714	14
88.	eArgbeuProdTyValtouSer

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aliqnment_block: 08 \cdot 09 \cdot 276 \cdot 935B \cdot 14 \times 08 \cdot 08 \cdot 649 \cdot 619B \cdot 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aliqnment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-649-619B-1
                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 477.50 Length: 497
Ratio: 1.844 Gaps: 18
Percent Similarity: 52.113 Percent Identity: 26.761
                                                                                                                                                                                                                                                                                    Aliquiseq 1/1 to: US-08-649-619B-1 from: 1 to: 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/INCRET NUMBER: FUTUYA CARO 1444
TELECO MMUNICATION INFORMATION:
IELEPINE: (616) 881 1156
TELEPINE: (616) 381-5465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CON-
ORIGINAL T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
356 GAGGCCAGCTCAGCCTGCAGCACAGACTGGGTCATCCCAGATCCCGAAGA 401
                                                                                                                                                                                         256 OCCCOMICAGOOTIGGCGCCCCCTTCTTCTTCACCCACTGTAAAGGAGGAGGAGG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: Human ma
LIBRARY: library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                           306 GLOCGGAGGCGTGGCCCGGGGGTCCGGACCCTGATGTCCCAGGCACTGAT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIPLE OF INVENTION: ENCODING THE SAME
                                                                                                                                19 pthroluserval.Prodly.....lysProSerValAsnAlaAspdlu 33
                                     44 GlaValGly.....
                                                                                                                                                                                                                                   5 ProfyschuserTrpAsnHisAlaAspPheValHisCysGlu.....As 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 206..1591
LDENTIFICATION METHOD: experimental examination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid STRANDEDNESS: double ToPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 21-SEP APPLICATION NUMBER: FILING DATE: 21-SEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homosapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP6-2:
FILING DATE: 21-SEPT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC/XT/AT Compatible OPERATING SYSTEM: MS-DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIRBET: 2026 Ran
CITY: Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Terryonce F. Chapman REGISTRATION NUMBER: 32549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/649,619B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STALE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49008 1699
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۲ 101	eAsnThrValPheAsnAlaGluThrGlvThrTrnGluCvs	288
0	CATCCACTATCGAGATCATGCTGCTAGAGA	103
90]n[]eSerLeuLeuLvs(]]vA aA]aPhe(]uLeuCvs(]nLeuArgP	272
271 1102	leSerPheAlaLysVallleSerTyrPheArgAspLeuProlleGluAsp:::::	255 .053
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	LeuLeuProHisMetAlaAspMetSerThrTyrMetPheLysGlyIle	238
		977
238	alTrpAsnTyrLysProProAlaAspSerGlyGlyLysGluIlePheS	222
7	.cTGGGCGCAGAC	Ō
	pLeuCysSerLeuLysValSerLeuGlnLeuArgGlyGluAspGl	
0	GACCAGCCCAAAGTCACGCCCTGGCCC	938
205	.laProSerArqGluGluAlaAlaLysTrpSerGlnValArgLy	188
937		937
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142		142
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120 705	SLYSCluMetIleMetSerAspCluAlaValG ::::::: ::::: ::: GGAGCAGTGCGTCCTTTCTGAAGAACAGATCC	10 4 656
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555	::::	506
_	lmetThrCvsGluGlvCvsLvsGlvPhePheArgArgAlametLvsA	
505	roGln IleCysArgValCysGlyAspLysAlaThrGlyTyrHisPheAsn roll IleCysArgValCysGlyAspLysAlaThrGlyTyrHisPheAsn roll Ill	38 456
	AACCAGAGEGCAAUCGAAAGAAGGGCCCAGCCCCGAAGATGCTGGG	

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	155 etAspAlaGlnMetLysThrPheAspThrThnPheSerHisPheLysAsn
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155	(lud)nArgMetMetIleArgGlub
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142	142
8 38	ADEDICACIONO ESPACIONA PEROPREDA EL
	137ProtengtyValGlnGTy
	745 GAAGAAGATTGUGAAAGAAGAAGAAGAAGAGGAGTGAGAGTGAGAGT
	120 uArgArgAldi.euflef.ysArgl.ysf.ysserdluArgThrd}yThrdIn.
744	WEDDOLENWING WEDWING ALLEGORD BANDOWS BY THE BENDANCE OF THE CONTROL OF THE CONTR
	645 ACRETTEDATERRACIONAACTRINOCACTORIONAACTRINOCATORIONAACTRINOCACTORIONAACTRINOCACTORIONAACTRINOCACTORIONAACTRINOCATORIONAACTRINOCATORIONAACTRINOCATORIONAACTRINOCATORIONAACTRINOCATURIOCACTRINOCATURIOCATURIOCAT
103	
644	71 qASBALIAATqLeuArgeysProPheArqLysGTyALiaCysGTuTLet
5.94	
7 1	AsviteMed Apakated (dvli)svitskipa (juli)svitation (dvli).
54 544	## roGIntleCysArqValCysGlyAsptysAlaThrGlyTyrHisPhoAsn
494	445 GRAM TAGAGEGCANGERIAANGANGGGGECCAGFEGEGGAAGATGETEGGGE
ŧ	ε7
444	44 CHARATETY
194	445 directional contrace coddddirectional central contraction and contraction
Ξ	19 pThrGluSerVall.ProditylysProSerVallAsnAlaAspGlu
19 344	5 ProfysdfuSerTrpAsnHisAlaAspPheValHisCysGluAs 19
	Align seq 1/1 to: US 08-330-518 1 from: 1 to: 2030
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	Ratio: 1.844 Gaps: 18 Percent Similarity: 52.114 Percent Identity: 26.761
	477.50 Length: 4
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1582	98 br	 55 4.
24.5	GEMANAGE IGEGOTTOCCGCGCATGCTCATGAAGCTGGTGAGCCTGCGCA	 4
1482	CACROCTAC TOTACA CACROCTAC ACACROCTAC ACACRACA CACROCTAC ACACROCTAC ACACRACA CACROCTAC	<u>.</u> 4
£ 4.52	Clud Luth (1111::H ::H ::: Cdaccdaecddcccaacdrocaddccdaadcerrorad Clud Luthoval a Llethr LeulysSerfyr Lled LutysasnArgtrod	1 181
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	33 uchlouhischuchuchufyrVallaumetchnlalteSerlouhes	
727.	17 GInLeuteuteudenGluproMetteutysPheHisTyrMetteutystyste ::::::::: ::::: 83 GTGGAGTTCATCAACCCCATCTTCCAGGTTCTGCGGGCCATGCGGCCT	12.
1282		302 1233
1242	eAsnThrValPheAsnAlaGluThrGlyThrTrpcluCys	111
1191	2 GIDTLESCRIEDLENLYSGI YALAALAPhed LILERCYSGI DIEDARGPH HILLER GITTELLE HILLER GITTELLER GIT	27 114
271 1141	5. FoSerPhoAlaLysValliloSerTyrPhoArqAspLouProilleGluAsp 	2) 10)
1.091	## rlandenProHisMetAlaAspMetSorThrTyrMetPholysGly11of	10
1050	22 ValTrpAsnTyrLysProProAlaAspSerdlyGlyLysGluTePheSe :: :::: ::: 	10
		10
221	splendysserizatlysValSerizathizatorqGlyGluAspGlySer	2
205 1004	8 uGhnAlakroSerArqGluGluAlaAlaLysTrpSerGluValArqLysA ::::::	18
476	976	بو
8.	${\it HI2-PheArgLeuProGlyValLeuSerSerGlyCysGluLeuProGluSerLe}$	_
476	## TGGCGGCCAACTGCAGTGCAACAAACGCTCCTCCC	ç

Seq.documentation_block:
; Sequence 1, Application US/08330283; Patent No. %679518
; GENERAL INFORMATION:

544	495 ACGAGCTTTGCCGTGTCTGTGGGGACAAGGCCTCCGGCTTCCACTACAAC
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38 494	37GlyP H
444	GAGGCCAGCTCAGCCTUCAGCACAGACTGGGTCATCCCAGA
36	34 GluValGly
33 394	19 pThrGluSerVal.ProGlyLysProSerValAsnAlaAspGlu ::: :::
19 344	5 ProLysGluSerTrpAsnHisAlaAspPheValHisCysGluAs
	Align seg 1/1 to: US-08-330-283-1 from: 1 to: 2030
	alignment_block: US-09-276-935B-14 x US-08-330-283-1
	alignment_scores: Quality: 477.50 Length: 497 Ratio: 1.844 Gaps: 18 Percent Similarity: 52.113 Percent Identity: 26.761
	SSS: Si Tinear PE: DNA L: NO NO
	⊢ - Ф
	OR SEQ ID NO:
	(908) 594-4283 (908) 594-4720
	-i
	ATTORNEY/AGENT INFORMATION: NAME: Dolan, Catherine A.
	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
	_
	NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
IATORS	
	APPLICANT: Holloway, M. Katharine APPLICANT: Rodan, Gideon
	APPLICANT: Friedman,

بد تد بدا	GlnLouLeuLouGluProMetLeuLvsPheHisTvrMetLeuLvsLvsLo	317
128	:::::: GANGGACTTCACCTACAGCAAGGACGACTTCCACCG	Les .
-	LeuSerTyrCysLeuGluAspThrAlaGlyGlyPheG	ö
301 123	eAsnThrValPheAsnAlaGluThrGlyThrTrpGluCys	288 1192
288 119	oSert.cut.eut.ysG1yA1aA1aPheG1ut.euCysG1nt.euArg 	4
271 114	heAlaLysValIleSerTyrPheArqAspLeo 	255 1092
255 109	uProHismetAlaAspMetSerThrTyrMetPhel 	238 1051
105	-pAsnTy	1016
0		0
221	$\verb pLeuCysSerLeuLysValSerLeuG \verb nLeuArgG y \verb G u \verb AspG y \verb serLeuG e u \verb ArgG y \verb G u \verb AspG y \verb serLeuG e u \verb ArgG y \verb serLeuG e u \verb ArgG y \verb g u \verb AspG y \verb serLeuG e u \verb ArgG y \verb g u \verb AspG y \verb serLeuG e u \verb ArgG y \verb g u \verb AspG y \verb g u \verb AspG y \verb serLeuG e u \verb g u \verb g u \verb g u u u u u u u u u u u u u u u u u u$	205
205 100	<pre>\laProSerArqGluGluAlaAlaLysTrpSerGlnValArqLy :::::: :::::::::::::::::::::::::::::</pre>	188 977
976		976
188	.euSerSerGlyCysGluLeuProGluSer	172
171 976	OMetLysThrPheAspThrThrPheSerHisPheLys ::::: AACTGCAGTGCAACAAACGCTCCTTCTCC	. 155 939
938		143 889
- D	TFCCCCTGGTGGATCTGAGGCAGGCAGCCAGGGCTCCGGGGAAC	نيا
142		142
142 838	######################################	137 789
136 788	<pre>\tqAlaLeu(LeLysArgLysLysSerGluArgThrGlyThrGl :: ::::::::::::::::::::::::::::::</pre>	120 745
4 K	LysLysGlumetIleMetScrAspGluAlaValGl ::::::::::::::::::::::::: :::: aGGGAGCAGTGCGTGCTTTCTGAAGAACAGATCCG	
103 694	SThrArqArqGinCysGlnAlaCysArqLeuArqLysCysLeu ::	87 645
87 6 44	PheArgLysGlyAlaCysGlulleT 	71 595
71 594	PheArgArgAlaMctLysAr 	545

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seq_name: /cqn2_6/ptodata/1/ina/5B_COMB.seq:US:08-646-248-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                        TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1434 CARROCTA/GTOGAGGCGCTGCTGTCCTA/CA/GGCGCATCAAGAGGCCGCA 1482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INM PC popartible
ODERALING SYSTEM: PC bos/MS bos
SOFTWARE: Patontin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1584 AAGAAGCTGCCGCCTCTCCTGCTGGGAGATCTGGGACGTC 1621
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                                                                                                                                                                                                                                                                 PILINE DATE: 27 OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dolan, Catherine A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Holloway, M. Kathu
APPLICANT: Rodan, Gldeon
APPLICANT: Rutledge, Su Jane
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/330,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 erProAspArqProGlyVallen@lnHisArqValValAsp@lnLenGln 366
                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Morck & Co., Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VogeL, Robert TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR PUTENTIATORS NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 .....ThrProLeuMetGlnGluLeuPheGlyIle 411
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                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
                                                                                                                                                                                                                           REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rahway
STRANDEDNESS: single
TOPOLOGY: linear
                                                  TYPE: nucleic acid
                                                                         LENGTH: 2030 base pairs
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938	CGAGGGTGTCCAGCTAACAGCGGCTCAAGAACTAATGATCCAGCAGCAGTTGG	688	
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1 36 788	UALGARGALALEULLELYSARGLYSLYSSERGLUARGTBRGLYTBRGLU.	120 745	
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103 694	hrarqlysFhrarqarqdIndysdInaladysArqLenarqlyscysLen 	87 645	
87 644	qAsnAlaArql.euArqCysProPheArqlysGlyAlaCysGlulleF 	71 595	
71 594	ValMetThrCysGluGlyCyslysGlyPhePheArqArqAlaMetLysAr :::::	545 545	
54 544	rodlnilerysArqValCysGlyAspLysAlaThrGlyTyrHisPheAsn 	48 495	
38 494	GDAAGCCAGAGAGAGGCGAAAGAAGAAGAAGGCCCCAGCCCGAAGATGCTGGGCC	445	
36 444	GLIVATIGETY	34 395	
394	pThroluserval.prodlyLysProServalAsnAlaAspGlu ::::::::::::::::::::::::::::::::::::	19 345	
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	eq 1/1 to: US-08-646-248-1 from: 1 to: 2	Aliqn s	
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	MOLDE OLLE TYPE: DNA (GEDOMIC) HYPOTHET LALE NO ANTESENSE: NO 08-646-248-1	: MOR ; HYP; ; ANI US-08-64	
	DNA CARRONNIA		

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seq_documentation_block:
   Sequence 1, Application PC/TUS9513924
;   GENERAL INFORMATION:
   APPLICANT: Friedman, Eitan
   APPLICANT: Holloway, M. Katharine
   APPLICANT: Rodan, Gideon
   APPLICANT: Rodan, Gideon
                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US95-13924-1
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       APPLICANT:
                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..........ThrProLeuMetGlnGluLeuPheGlyIle 411
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Holloway, M. Katharine
Rodan, Gideon
Rutledge, Su Jane
Schmidt, Azriel
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seq 1/1 to: PCT-US95-13924-1 from: 1 to: 2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (908) 594-4/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Quagliato, Carol S.
REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 19327 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                          445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Quagliato, Carol S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                        395
                                                                                                                                                                                                                                                                                                                                                                       345 GTCCGGAGCCGTGGCCCGGGGGTCCGGACCCTGATGTCCCAGGCACTGAT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 CCCCCCTCAGCCTGGCGCCCCTCTTCTTCACCCACTGTAAAGGAGGAGG
                                                                                                                                                                                                                                                                                                                                 34 GluValGly.....
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
71 qAsnAlaArqLenArqCysProPheArg...LysGlyAlaCysGlulleT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 ProLysGluSerTrpAsnHisAlaAspPheValHisCysGlu.....As 19
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (908) 594-3809
TELEFAX: (908) 594-4720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                        GTGCTCAGCTGCGAAGGCTGCAAGGGCTTCTTCCGGCGCAGTGTGGTCCG
                                                                                                                                                                                                                                                                                        GAGGCCAGCTCAGCCTGCAGCACACACTGGGTCATCCCAGATCCCGAAGA 444
                                                                              ValMetThrCysGluGlyCysLysGlyPhePheArgArgAlaMetLysAr 71
                                                                                                                         ACCAGCTTTGCCGTGTCTGTGGGGACAAGGCCTCCGGCTTCCACTACAAC
                                                                                                                                              roGlnIleCysArgValCysGlyAspLysAlaThrGlyTyrHisPheAsn 54
                                                                                                                                                                                                          GGAACCAGAGCGCAAGCGAAAGAAGGGCCCCAGCCCCGAAGATGCTGGGCC
                                                                                                                                                                                                                                        Quality:
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126 East Lincoln Av
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52.113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/US95/13924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 18
Percent Identity: 26.761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                           544
                                                                                                                                                                                                          494
                                                                                                                                                                                                                                                                                                                               36
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\$ 50	uClnLouffisGluCluCluTyrValLeuMetClnAlatleSerteuPheS	3
1 3 3 2	## GEGGAGTECATCAAGCCGATCTTGGAGTTCTGGGGGGGGGG	7 H 2
÷	GlinLeuLeuChuProMetLeuLysPheHisTyrMetLeuLysLysLe	317
1282	TGAAGTACTTCACCTACAGCAAGGAAGGACGATTCCAACCGTGAAGCTGCAAG	÷ .
- 16	GlyArgLouSerTyrCystauGluAspThrAlaGlyGlyBbeGln	302
1232	ASSERTING A STREET OF THE TOTAL OF THE STREET OF THE STREE	76.1
Ê	oAsnThrValPhoAsnAlaGluThrGlyThrTrpCloCys	882
1151	CANTATO COCCOCTICA AGGACTA OCCACTATO CACATO A TOTATO AGAIN.	142
2 F	Challeson tendentant vs81 vAlaALphothus to averanos entropedo.	273
271	1eSer PheAlaLysVali LeSer TyrPheAr (ASpLeuPro LleGtuAspleu Linder)	255
1091	CCACTICACGAMACIGACATCATCACTCACTCAGAGAGATCG	15.0
255	rLeuLeuProHisMetAlaAspMetSerThrTyrMetPheLysGlyTleT	81.7
1050	THE THE TENT OF THE PROPERTY O	016
238	ValTrpAsuTyrLysProProAlaAspSerGlyGlyLysGhullePheSe	2.22
1015	CTGGGCGCAGAG	004
221	splouCysSerLeuLysValSerLeuGlnLeuArqGlyGluAspGlySer	205
1004	GARCAGCCAAAGFCACGCCCGCCCC	177
205	aGInAlaProSerArqGluGluAlaAlaDySTrpSerGluValArqLysA	Ŧ
976		976
88	Phe A red Leu Ser Ser Gly Cys Glu Leu Pro Glu Ser Le	172
976	TGGCCGCCCAACTGCAGTGCAACAAACGCTCCTCTCTCCC	4.5.6
171	etAspAlaGlaMetLysThrPheAspThrThrPheSerHisPheLysAsn	155
88.6	CGAGGGTGTGCGAGCTAACAGCGGGTCAAGAACFAATGATCCAGCAGTTGG	£ # #
155	LeuThrGluGluGlnArgMet Met HeArgGluLeuM	4.
888	${\tt GGGGGCTTTCCCCCTGGTTGAGTCTAGGGGAGGGAGGGAG$	3
142		4.2
π π	COCACTOTOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOC	789
142		1.17
788	GANIAAGATECGGAAACAGCAGCAGAGAGCACAGFCACAGFCACAGF	745
136	uArqArqAlaLouLloLysArqLysLysSorGluArgThrGlyThrGln.	07.1
744		569
120	GinserGlyMetLystysGluMetILeMetSerAspGluAlaValGluGl	0.4
694	ACGCTTTCATGCGGCGCAAGTGCCAAGCAGTGCCAAGTGCAAAG	645
<u>.</u>	hrArat.vs:thrAraAraGlmCvsGlmAtaCysArat.vuArat.vsCyst.ou	в7
644	TGGTGGGGGCAGGGGTATGCCTGCCGGGGGGAAACCTGCCAGATGG	262

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aliqnment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /eqn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US95-18941-1
                    Ratio: 1.844
Percent Similarity: 52.113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9518931
GENERAL INFORMATION:
APPLICANT: Firefman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Rodan, Gideon
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 - AAGAAGCTGCCGCTCTCCCTCTCGGAGATCTGGGACGTC 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1533 СОСТОЛОСТ СТСТССАСТСЕСВАССАССТСТССССТТСССССТСССАССАС 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 F GUACCAGUTUUGGUTTCUCGGGGATGCTCATGAAGUTGGTGAGGUTGCGGA 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1433 CAGCCCTACCITGGAGGCGCTGCCCTACACGCGCCATCAAGAGGCCGCA 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1383 COGCCGACCGGCCAACGTGCAGGAGCCGGGCCGCGTGGAGGCGTTGCAG 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1333 GGGCCTGGACGAGGCTGAGTACGCCCTGCTCATCGCCATCAACATCTTCT 1382
                                                                                                                                                                                                                    HYPOTHETTOAL: NO
HYPOTHETTOAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUSTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 .....ThrProLeuMetGlnGluLeuPheGlyIle 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 mProAlaHisArqPhe....LemPheLemLysTleMetAlaMetLemT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 GludinPheAlaIleThrLenLysSerTyrlleGludysAsnArdProof 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 erProAspArqProGlyValLeuGlnHisArqValValAspGlnLeuGln 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 126 E
CITY: Rahway
STATE: New Je
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Quadiliato, Carol S.
REGISTRATION NUMBER: 45,330
REFERENCE/INCKET NUMBER: 19416 PCT
                                                                                                                                                                                                                                                                                            LENGTH: 2030 base pairs
TYPE: nucleic acid
SIRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/13931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                     guality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07065-0907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE: Merck & Co., Inc.
126 East Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SII
                                                                                                                                                                                                                                                                                                                                                                                                                                              (908) 594-3809
                                                                                                                                                                                                                                              DNA (genomic)
                                                                     477.50
Gaps: 18
Percent Identity: 26.761
                                                                        Length:
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ANGGAGG ANGGAGGA COGAAGA COGAAGA COGAAGA COGTCGG TACAAGC TACACAGT TACAAGC TACACAGT
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222 ValitpAsinTytLysProtrahlaaspScrid VolyLyspithuiteithese 238 1016

2 2	CMPUTER: IBM PC compatible	
	OFTERMARE: Patentin Release #1.0, Version #1.30	
ू इ. <u>१</u>	TITING PARE: 18 NOV 1994	
VI.1.V	"GASSIFICATION: 435"	
- Z Z	DESTRATION NUMBER: 83,928	
# ### ####	REFERENCE/DOCKET NUMBER: ARCHINA TELEPIENNE: (512) 41H - JUDO TELEPIENNE: (512) 41H - JUDO	
= = :	ELEFAX: (7) 8) 789-2679 ELEX: 79 0924	
INFOR	MATION FOR SECTIONS: 1:	
∃ E	ENGIH: 1898 base pairs YPE: metele acid	
글 약	TRANDEDNESS: Single	
FEA:	ATTIRE:	
08 · 44:	100X(100) 711450 1042 411A-1	
iqument	Sectors:	
61 COUT	1.849 Gaps: 51.911 Percent Identity: 26.	
	olock: 935B-14-x-US-08-342-411A-1	
lign s	n seq 1/1 to: US-08-342-411A l trom: 1 to: 1898	
H 7	ProLysCluSerTrpAsnHisAlJAspPheValHisCysCluAs []]	15
148	pffhrefluSerVal .Prodlytys)roSerValAsnAlaAspdlu ::: ::: :::::::::::::::::::::::::::::	2 -
218	CLIVALIGEY	6 5
47		Œ
268	F GDAACCAGAGCGCAAGAGAAGAAGGAGCCCAGCCCGAGGATGCTGGGGC - { }	-
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\$58 \$5	VALMOOTTHECYSGLOGLYCYSLYSGLYPHOPHOAFGARGALAMOOLYSAE 71 	
71		6.
87 468		- 0
104	GIUSerGlyMetLystlysGluMetlleMetSerAspGluAlaValGluGl 	£ 12

Ē	3 nProAlaHisArgPhebeuPhebeubysHeMetAlaMetbeul	æ
1305		1256
£	olio Jin Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala He Thr Leu Lys Ser Tyr He Glu Cys As i Arq Proposition (Ala Phe Ala	367
466 1255	0 erProAspArqProGLyValLeudInBisArqValValAspGInLeudIn 	1206
150 1205	UST ELEMBIS SCHOOL UST TYPVALLEM MET GENALATE	9511
1155	dIntententendinPromettentysPheHisTyrMettentysLysta- :::::::	317 1105
316	GlyArqLeuSerTyrCysLeuGluAspThrAlaG ::::::!!! TGAAGGACTTCAGCTACAGGAAGGACGACTTCCACCGTG	302 1056
1055	eAsnThrValPheAsnAladluThrGlyThrTrpGlucys :::III	1015
← N.1	GlmileSerLeuLeutysGlyAlaAlaPhedl 	272 965
271 964	LeSerPheAl-dtysVallLeSerTyrPheArqAspteuProlleGluAsp :::::HHHHHH	516 527
255 914	rleuleuProHisMetAlaAspMetSerThrTyrMetPheLysGlyllel 	248 874
238 873	ValTipAshTyrLysProProAlaAspSerGlydlyLysGluiloPhese	222 839
± 1	CTGGGGCAGAC	827
		505 008
502	uclnAlaProSerArqCluGluAlaAlaLySTrpSerGlu	188
	PheArdLoubrodTyValLouSerSerdTycysdTuLoubrodTuSor	172
171 799	et AspAl ad LiMet LysThrPheAspThrThrPheSerHisPheLysAsii ::	155 762
		143 712
711	GGGGCTTCCCCTGGTGGAFCTGAGGCAGGCAGGCAGGGCTCCGGGGAAAGG	662
142		142
142 661		137
136 611	uArqArqAlaLeulletysArqLystysSerGluArqThrdlyThrGlu.	120 568

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